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GenCore version 5.1.6
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OM hucleic - nı	OM hucleic - nucleic search, using sw model
Run on:	<pre>September 5, 2003, 07:20:00 ; Search time 1677 Seconds (without alignments) 9660.234 Million cell updates/sec</pre>
Title: Perfect score: Sequence:	US-09-684-215A-3 396 1 acggccgcgtccgataactttggccgaggacccccggcc 396
Scoring table:	IDENTITY_NUC

2888711 seqs, 20454813386 residues Gapop 10.0 , Gapext 1.0 Searched:

5777422 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

9b\_htg: 9b\_nn:\* 9b\_om:\* 9b\_pat:\* 9b\_pl:\* 9b\_pr:\* 9b\_pr:\* 9b\_sy:\* 9b\_sy:\* 9b\_vi:\* em\_ba:\* em\_fun:\* em\_hum:\* em\_om: em\_ov: GenEmbl:\* Database :

em\_htg\_inv:\* em\_htg\_other:\* em\_htg\_mam:\* em\_htg\_vrt:\* em\_sy:\* em\_htg\_hum:\* em\_htg\_pln:\* em\_htg\_rod:\* em\_htg\_mus:\* em\_pat: em\_ro:

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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22	91.	æ	^	φ	BD069298	98	Compounds
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24	S	6	7	9	_	49	Sequence
25	S	6	7	9	_	148	Sequence
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38	S	9	15	9	10	5916	Sequence
39	S	9	0	٥	101	1107	Sequence
40	S	c.	20	9	5787	5787	Sequence
41	S	6	46	9	2941	41	Sequence
42	S	g,	46	ဖ	5610	5610	Sequence
43	S	0	46	9	6195	5195	Sequence
44	S	Ç.	55	9	39	2939	Sequence
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## ALIGNMENTS

RESULT 1			
rocus	AX005788 1068 bp DNA	linear	PAT 24-AUG-200(
DEFINITION	Sequence 907 from Patent WO9909186.		
ACCESSION	AX005788 .		
VERSION	AX005788.1 GI:9928795		
KEYWORDS			
SOURCE	Mycobacterium tuberculosis		
ORGANISM	Mycobacterium tuberculosis		
	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	Actinom	ycetales;
	Corynehacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium	acterium;	Mycobacterium
	tuberculosis complex.		

PAT 24-AUG-2000

Portnoi, D. and Guigueno, A. Polypeptide nucleic sequences exported from  $\operatorname{\mathsf{mycobacteria}}$  , vectors

REFERENCE AUTHORS TITLE

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1 ACGGCCGCGT
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FPALPLPPSAWVAQVGPOVVNINTKLGYNNAVGAGTGIVDDNGVVLTNNHVIAGATD
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NNGNARVQRVVGSAPAASLGISTGDVITAVDGAPINSATAMADALNGHHPGDVISVT
MGTKSGGTRTGNVTLAEGPPA
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Polypeptide nucleic sequences exported from mycobacteria, vectors
comprising same and uses for diagnosing and preventing tuberculosis
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium, Mycobacterium
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/mol_type="genomic DNA"
/db_xref="taxon:1773"
1..1068
            and
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         same and uses for diagnosing 9909186-A 907 25-FEB-1999;
comprising same and usc.
Patent: WO 9909186-A 907 25-FEB-1999,
PORTNOI DENIS (FR); GUIGUENO AGNES (FR)
Location/Qualifiers
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/protein_id="CAC05178.1"
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Fusion proteins of mycobacterium tuberculosis antigens and their
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11arity 100.0%; Pred. No. 4.2e-57;
Conservative 0; Mismatches 0;
WO 9903186-A 909 23-rrb 11.0 GFR); GUIGUENO AGNES (FR) LOCALLON/Qualiflers
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Location/Qualifiers
1. . . 2287
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rom patent US 6544522.
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/note="Rv0119, (MTV031.13-MTC1418B.01), len: 525.fadb7, possibleCoenzyme A-ligase similar to 4-coumarate.CoA ligase of manyorganisms e.g. pru039405_1 (537 aa). Contains pS00455putative AMP-binding domain signature. FASTA scores: gp1039405|pr039405_1 Pins taeda xylem 4-coumarate:CoA (537 aa) opt:4832-score: 526.1 E(): 8.3e-22; 28.2% identity in 440 aaoverlap score is 0.896"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGHGLIASLLATLASGGAVSLPARGRESAHTFWDDIKAVGATWYTAVPTIHQILLERS
ATEPSGRKPAALRFIRSCSAPLTAQAALALQTEFAAPVVCAFGMTEATHQVTTTQIEG
IDQTETPVVSTGLVGRSTGAQIRIVGSDGLPLPAGAVGEIWLRGTTVVRGYLGDPTIT
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/LIVMFY].[2][STG][STAG]G[ST][STEI][SG].[PASLIVM][KR], info
count = 22.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAB09455.1"
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/db_xref="SPTREMBL:007169"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DELAGQLTRSGLLPGDRVALRMGSNAEFVVALLAASRADLVVVPLDPALPITEQRYRS
QAAGARVVLIDADGPHDRAEPTTRWWPLTVNVGGDSGPSGGTLSVHLDAATEPNPATS
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AVFGVPHQLYGEAVAAVIVPRESAPPTREELVOFCRERLAAFEIPASFQEASGLPHTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPEGLRPDDAMIMFTGGTTGLPKMVPWTHANIASSVRAIITGYRLSPRDATVAVMPLY
                                                                     URE, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, oft, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="fragment designated v031. Does not represent a
                           Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mycobacterium tuberculosis H37Rv"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .11700
/organism="Mycobacterium tuberculosis H37Rv"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="H37Rv"
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                                                     available on the World Wide Web
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:83332"
1309. .11293
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/product="fadb7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="H37Rv"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="I418B'
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97. .1674
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                                                                                                                                                                                                                                               ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGCCAACGGCGCACGA 180
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Harris, D., Gordon, S.V., Eiglmeler, K., Gas, S., Barry III, C.E.,
Tekala, F., Badocock, K., Basham, D., Brown, D., Chillingworth, T.,
Connor, R., Davles, R., Devlin, K., Feltwell, T., Gentles, S.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krofn, A., McLean, J.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
Barrell, B.G.
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACACGGCAACGGCGCACGA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCAACGCGTGGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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                                                                                                                                                            Gaps
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                                                                                                          Length 2287;
                           3 others
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                                                                                                       100.0%; Score 396; DB 6; 100.0%; Pred. No. 3.7e-57;
                           ų
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Nature 393 (6685), 537-544 (1998)
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/organism-"unknown"
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                                                                                                          Query Match
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DEFINITION
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VERSION
KEYWORDS
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JOURNAL
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MEDLINE
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Mycobacterium tuberculosis CDC1551
Mycobacterium tuberculosis CDC1551
Bacteria, Accinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
1 (bases 1 (c) 14029)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Folnowy, J.F., Nablson, W.C., Umayam, L.A., Ermolaeva, M.,
Salzberg, S. Lo, Delcher, A., Utterback, T., Weidman, J., Khouri, H.,
Gill, J., Mikula, A. and Bishai, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGTCGGGAGCGCTCCGGCGCCAAGTCTCGGCATCTCCACCGGCGACGTG
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complete genome.
AE006925 AE000516
AE006925.1 GI:13879610
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Best Local Similarity
Matches 396; Conserv
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AE006925
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Rv0120c, (MTC1418B.02c), fusA2, len: 714.
Elongation factor g, similar to eg. EFG_ECOLI P02996
elongation factor g (ef-g). Escherichia coll (703 aa),
fasta scores; opt:1049 z-score: 1105.5 E(): 0, 32.58
identity in 717 aa overlap. Contains PS00017
ATP/GTP-binding site motif A (P-loop). Also similar to M.
tuberculosis fusA, MTCY210.01 (39.1% identity in 299 aa
overlap). Similar to spip307671BFG_MYCLE ELONGATION FACTOR
G (EF-G). (701 aa); 31.7% identity in 710 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"hypothetical protein Rv0121c"
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/db_xref="G1:2181963"
/db_xref="SPTREMBL:007171"
/db_xref="SPTREMBL:007171"
/db_xref-"SPTREMBL:007171"
/db_xref-"SPTREMBL:00
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HTRGVQRVRVTRNARKHRVSKHRIVAAMRHCGVPVIQEDGSLYYQGRDTSGRLTEVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PS00017 ATP/GTP-binding site motif A (P-loop)" complement(3956. 4390) /gene="Rv0121c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aa 
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/transl_table=11
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/gene="Rv0121c"
/note="Rv0121c," (WTC1418B.03c), unknown, len: 144
/codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="possible RBS upstream of Rv0121c" 4532, .4535
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/note="possible RBS upstream of Rv0122"
4539. .4907
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1904. .5272
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/db_xref="SWISS-PROT:007170"
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          complement(1675. .3819)
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/product="fusA2"
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/gene="Rv0123"
4904. .5272
/gene="Rv0123"
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/gene="Rv0122"
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/gene="Rv0122"
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8044

180

120

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8104

300

240

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similarity; putative"

//codon_start=1

/transl_table=11

/product="alpha-amylase family protein"

/protein_id="AaAk43581"

/db_xref="al.19879616"

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RANYEVELVRAFFDASABGSOBLRGIDRLDYLOYLOWIGTOTRAPPFYDFLRGGYV

IRDFYKVLPEFGTYDDPVALVAARRGIRITYDLUNNHITSESHPWPGESREDPDGFY

GDYYVWSDTSERYTDARIIFVDTEESNWSFDPVRQFYWHRFFSHQPDLNYDDAVQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INAFSVGSGQTYGVDVVGYDRTQDVAVLQLRGAGGLPSAAIGGGVAVGEPVVAMGNSG
GQGTPRAVPCRVVALGGTVQASDSILGAEETINGILQFDAALQPGDSGSGPVVNGLGQ
VVGNNTAASDNFQLSQGGQGFAIPIGQAMÄIAGQIRSGGGSPTVVIGPTAFLGLGVVD
NNGNCARVQRVVGSPAASIGISTGDVITAVDGAPINSATAMADALNGHHPGDVISYT
WQTKSGGTRTGNVTLAEGPPA
                                   QGAGGGAGGAGGAGGAGAGRGLWGTGGAGGHGGQGGGTGGPPLPGQAGWGAAGGAGG
LIGNGGAGGDGGVGASGGVAGVXGAGGNAMLIGHGGAGGAGGDSSFANGAAGGAGGAG
                                                                                     GHLFCNGGSGGHGGAVTAGNTGIGGAGGVGGDARLIGHGGAGGAGGDRAGALVGRDGG
PGGNGGAGGQLYGNGGDGGPGGPGGAGGARGANNIGGTGGAGGNGGPAILSGNGGNGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSNSRRSLRWSWLLSVLAAVGLGLATAPAQAAPPALSQDRFAD
FPALPLDPSAMVAQVGPQVVNINTKLGYNNAVGAGTGIVIDPNGVVLTNNHVIAGATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDVIRFWIGLGIDGFRLDAVPYLFFREGTNCENLPETHAFLKRVRKVVDDEFPGRV
LLAEANQWPGDVVEYFGDPNTGGDECHMAFHFPLMPRIFMAVRRESRFFISEIIAQTP
PIPDMAQWGIFLRNHDELTLEMVTDEFRDYMYAEYAKDPRMKANVGIRRRLAPLLDND
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SCHYLLPSGODPYYGYQAWVPRAGNTSTSLLLHSTRYMLAVRRHPAFRYGRLGG
SURSYLAYVRQVAGDDGDTVLCVNNLSRFPQPIELDLQQWTNYTPVELTGHVEFPRIG
QVPYLLTLPGHGFYWPQLTTHEVGAPPTCGGERRL"
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LLSLIVSSAVČGTSTGEVTFTREPDVELPFAAQPRVCDAEQSNTSVIFDRRAILKVFR
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AEGWAMATASVRDLFAEGDLYAHEVGGDFAGESYRLGEAVASVHATLADSLGTAQATF
PVDRMLARLSSTVAVVPELREYAPTIEQQFQKLAAEAITVQRVHGDLHLGQVLRTPES
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VERNRAAFCDGYAVASGIDPRDSALLLGAYELDKAVYETGYETRHRPGWLPIPLRSIA
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     3HGGAGGAAGLWGAGGGGGGNGADANIVSGGDGGLGGAGGGGGWLYGDGGAGGHGG
                                                                                                                                             GAGGAGGAGGAGGAGGAPGTGGTLQAAVSGLVTALFGAPGQPGDTGQPG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GP:2808807; identified by sequence
                                                                                                                                                                                                                                                                                        /note="identified by match to protein family HMM"
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                                                                                                                                                                                                                                                                                                                                                                       /product="serine protease, putative"
/protein_id="AAK44357.1"
/db_xref="G1:13879615"
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/protein_id="AAK44359.1"
/db_xref="G1:13879617"
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/codon_start=1
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/gene="MT0134"
4695. .6500
/gene="MT0134"
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/gene="MT0136"
8038. .8817
/gene="MT0136"
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/gene="MT0133"
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/gene="MT0135"
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/gene="MT0135"
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/gene="MT0133"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MASSSSLPLLRHCVSDDQVTVVGFDGDDLGKTARRIAALVVQRA
IFENDRNTAVAHSGDDAVLGHAVLPGYPRDPDPLHASSMYSILGMCQSVNGRPFDAIA
IVSVRLCHVAVTDPTDSCGGRDRPGQLPCAPLDYHRHH"
1047. .1415
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ASESLRLAREREANLIPGGKSLSGGSAHSPAVQVVVSKATHAKLKELARSRKMSVSKL
LRPVLDEFVQRETGRILPRR"
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AAAAPTTAVLAAGADEVSAAIAALESGHAQAYQALSAQAAAFHQQFVQTLAGGAGAYA
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AGQAGGAGGPAGLIGHGGSGGAGGSGAAGGGGGGHGWLWGNGGVGSGGAGVGAGVA
Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                               'Eleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Salzberg, S.L., Mikula, A. and Bishai, W.
Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockviile, MD 20850, USA
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/gene="MT0131"
/note="identified by match to protein family HMM"
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mycobacterium tuberculosis CDC1551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product-"DNA-binding protein, CopG family"
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'db_xref-"GI:13879613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="identified by Glimmer2; putative"
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gene="Mn0110"
/note="identified by Glimmer2; putative"
/codon_start="
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                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
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/transl_table=11
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1682. .3367
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/note="Mb0001, dnaA, len: 507 aa. Equivalent to Rv0001,
len: 507 aa, from Mycobacterium tuberculosis strain H37Rv,
(99.6% identity in 507 aa overlap). dnaA, chromosomal
replication initiator protein (see citations below),
equivalent to other Mycobacterial CHROMOSOMAL REPLICATION
INTITATOR PROTEINS e.g. 1946388|DNAA_MYCLE from
Mycobacterium ieprae (502 aa); 09L7L71DNAA_MYCPA from
Mycobacterium paratuberculosis (509 aa); P49990|DNAA_MYCAV
from Mycobacterium smegmatis (504 aa); etc. Also highly similar
to others except in N-terminus e.g. 09ZH75|DNAA_STRCH
CHROMOSOMAL REPLICATION INITIATOR PROTEIN from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire
Bacterienne Institut Pasteur 28, rue du Dr Roux 75724 PARIS cedex
Bacterienne Institut Pasteur 28, rue du Dr Roux 75724 PARIS cedex
Bacterienne Institut Pasteur is Submitted on behalf of the
Mycobacterium bovis sequencing teams, TB Research Group, Veterinary
Laboratories Agency Weybridge, Woodham Lane, New Haw, Addlesstone,
Surrey KT15 3NB, UK. Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA, UK. PT4 Annotation, Genopole, Institut
Pasteur, 28 Rue du Docteur Roux, 75724 Paris Cedex 15, France.
rue du Docteur Roux, 75724 Paris Cedex 15, France
           BX248334 343050 bp DNA linear BCT 11-JUN-2003 Mycobacterium bovis subsp. bovis AF2122/97 complete genome; segment
                                                                                                                                                                                                                                                                                                                                                                                                                                             Garnier, T., Eiglmeier, K., Camus, J.-C., Medina, N., Mansoor, H., Pryor, M., Uuthoy, S., Grondin, S., Larcolak, C., Monsempe, C., Simon, S., Harris, B., Atkin, R., Doggett, J., Mayes, R., Keating, L., Wheeler, P.R., Parkhill, J., Barrell, B.G., Cole, S.T., Gordon, S.V. and
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Streptomyces reticuli (643 aa); DNAA_ECOLI|P03004|B3702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNAA"
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       BCT 11-JUN-2003
                                                                                                                                                                                                                          Mycobacterium bovis subsp. bovis AF2122/97
Mycobacterium bovis subsp. bovis AF2122/97
Bacteria; Actinobacteria; Carinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mycobacterium bovis subsp. bovis AF2122/97"
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/strain="AF2122/97"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The complete genome sequence of Mycobacterium bovis online Publication Physication Physication ( Microbiology ) 2 (bases 1 to 343050)
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1. .343050
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1. .1524
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                                                                                                             BX248334 BX248333
BX248334.1 GI:31616762
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                                                                                                                                                                                                                                                                                                                                                                             tuberculosis complex.
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GVDIMLGGWHESMLDFVPILFVVFGIGALNTSFVKDGEVSVPLSYVTGTLVKMGQGIE
                                                                                                                                                                         RHLAGGKVEDWLGYFLLHASFVLGAAAGGAISMVYTGPQMLAVAAVVCAATTGYTYLH
ADRRGLVNQKRPQPGKRLFRALRRGELDSGTSTPATNYGSS"
COMPlement(8949. .9989)
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INTPAFEEYYOSGLSVIMPVGGOSSFYTDMYOPSOGNGNYTYKWETELTREMPAWLO
ANKOVSPTGNAAVGLSMSGGSALILAAY PROOFFYAASLSGENDSEGWPPTLIGLAM
NDSGGYNANSWMGPSSPARAKUNDEWVOIPPLANDYNYTHWYYCGNTPSDLGGDNIPA
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                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to SP:P31953 GB:X57229 PID:48828
PID:1567734 PID:1877254; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="nodulation protein N-related protein"
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/db_xref="GI:13879620":
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Best Local Similarity 100.0%; Pred. No. 2.6e-57;
Matches 396; Conservative 0; Mismatches 0;
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/transl_table=11
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10218. .10673
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/goue_tag="Mb0002"
2052. 3260
/goue_tag="Mb0002"
/locus_tag="Mb0002"
/locus_tag="Mb0002"
/focus_tag="Mb0002"
/focus_tag="Mb0002, dnaN, len: 402 aa. Equivalent to Rv0002, len: 402 aa, from Mycobacterium tuberculosis strain H37Rv, (99.8% identity in 402 aa overlap). dnaN, DNA polymerase III (beta chain) (EC 2.7.7.7) (see citations below). equivalent to other Mycobacterial DNA POLYMERASES III BETA CHAIN e.g. NP_301130.1|NC_002677 from Mycobacterium leprae (399 aa); Q917.6|DP3B_MYCPA from Mycobacterium avium subsp. paratuberculosis (399 aa); P52851|DP3B_MYCSM from Mycobacterium segmatis (397 aa); etc. Also highly similar to others e.g. P27903|DP3B_STRCO DNA POLYMERASE III BETA CHAIN from Streptomyces coelicolor (376 aa); FASTA scores: opt: 1189, EC: 00, (52.8% identity in 337 aa overlapp); P52023|DP3B_SYNP7 from Mycrococcus luteus (310 aa); P52023|DP3B_SYNP7 from Synechococcus sp. strain PCC 7942 (375 aa); etc. Overlaps and extends CDS in neighbouring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Jocus_tag="Mb0003"
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/Jocus_tag="Mb0003"
/Jocus_tag="Mb0003"
/Jocus_tag="Mb0003"
Jen: 385 aa, from Mycobacterium tuberulosis strain H37Rv, 189.5% identity in 385 aa overlap). reck, DNA replication and repair protein (see citations below), equivalent to others Mycobacterial DNA replication and repair protein (see citations below), equivalent to others Mycobacterium DNA replication and repair proteins e.g. NP_301131.1\", C_002677 from Mycobacterium.leprae (385 aa); ps012151ERCF_MYCPA from Mycobacterium avium subsp. paratuberculosis (384 aa); etc. Also highly similar to others e.g. P361761ERCF_STRCD DNA REPLICATION AND REPAIR PROTEIN from Streeptomyces coelicolor (373 aa); NP_440892.1\", NC_000911 from Synechocystis sp. strain PCC 6803 (384 aa); NP_469352.1\", NC_00312 from Listeria innocua (370 aa); etc. Contains PS00017 AFP/GTP-binding site motif A (P-loop), PS00617 RecF FAMILY."
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LPMLTGIRVEILGETVYLAATDREFILAVREIKWSASSDDIEJAAVLYPAKTIARAAKAG
IGGSDVRLSLGTGFGVGKDGLLGISGNGKRSTTRLLDAEFPKFRQLLPTEHTAVATMD
VAELLEATKLYALVADRGAQVRMEFADGSVRLSAGADDVGRAEEDLYVDYAGEPLTIA
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YLLMPVRLPG"
3280. .4437
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                                                                                                                                                                  EGKEGIQEEFFHTFNTLHNANKQIVISSDRPPKQLATLEDRLRTRFEWGLITDVQPPE
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HAAGNYAQRLFPGMRVKYVSTEEFTNDFINSLRDDRKVAFKRSYRDVDVLLVDDIQFI
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EGNRVALTCGNARFSLPTMPVEDYPTLPTEFTGLLPAELFAEAISQVAIAAGRDDT
RAWLNLVQPLTIVEGFALLSVPSSFVQNEIERHLRAPITDALSRRLGHQIQLGVRIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="DNA POLYMERASE III (BETA CHAIN) DNAN (DNA NUCLEOTIDYLTRANSFERASE)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAD92864.1"
/db_xref="G1:31616764"
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'qene="dnaN"
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/dous_tag="Mb0004"
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/note="Mb0004, -, len: 187 aa. Equivalent to Rv0004, len:
/note="Mb0004, -, len: 187 aa. Equivalent to Rv0004, len:
/note="Mb0004, -, len: 187 aa. Equivalent HJRv.
/gy-5% identity in 187 aa overlap). Conserved hypothetical
protein (see citation below), highly similar, but longer
21 aa in N-terminus, to AAP35965.1AF222789 unknown
protein from Wycobacterium avium subsp. paratuberculosis
/166 aa); and highly similar to NP_30113.1INC_002677
conserved hypothetical protein from Mycobacterium leprae
/189 aa); 570990 hypothetical protein from Mycobacterium
smegmatis (194 aa). Also similar to in C-terminus to
C-terminal part of P35925|rREG_STRCO HYPOTHETICAL 19.8 KDA
PROTEIN (IN RECF-CYRB INTERCENIC REGION) from Streptomyces
collicolor (190 aa), FASTA scores: opt: 404, E(): 3.9e-18,
/codon_start=1
//codon_start=1
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/Jours_197="Mb0005"
/Jours_197="Mb0005, gyrB, len: 714 aa. Equivalent to Rv0005, note="Mb0005, gyrB, len: 714 aa. from Mycobacterium tuberculosis strain H37Rv, (99.9% identity in 714 aa overlap). gyrB, DNA gyrase subunit B (EC 5.99.1.3) (see citations below), equivalent, except in N-terminus, to other Mycobacterial DNA GYRASES SUBUNIT B eg. T10005 from Mycobacterium leprae (697 aa); Q91713|GYRB_MYCPA from Mycobacterium avium subsp. paratuberculosis (677 aa) (has its N-terminus shorter); P48355|GYRB_MYCSM from Mycobacterium smegmatis (675 aa); etc. Also highly similar to others e.g. T10969 from Streptomyces coelicolor (686 aa); P50075|GYBS_STRSH from.
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TRALLKSVGPGCARROPTOLEVWDRSLABERGELVAARTDLVVOLAPEVKRAYOL
LAPESRSASIGYRASHOVTGPSGOSDTDRQLLAARLLAALAARRDAELERSVCLVGPH
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/db_xref="G1:31616765"
/translation="MYVRHLGLRDFRSWACVDLELHPGRTVFVGPNGYGKTNLIEALM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RGRVASVASGRVAGRRRSWSGPGPDIRDPQPLGKAARELAKKRGWSVRVAEGMVLGOM
SAVVGHQIAEHARPTALNDGVLSVIAESTAMATQLRIMQAQLLAKIAAAVGNDVVRSL
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                                                              YSTTLGSHRVSADLPLIRVGTDRAVISTIVVNDGRECAVDLEIATGRVNKARLNRSSV
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/protein_id-"CAD92866.1"
/db_xref-"GI:31616766"
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5123. .7267
/gene="gyrB"
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123. .7267
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1 (bases 1 to 447)
Reed.S.G., SKelky,Y.A.W. and Dillon,D.C.
Compositions and methods for the prevention and treatment of M.
tuberculosis finfection
Patent: US 6350456-A 4 26-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 ACGGCCGCGT@CGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                             191 GTCCAACGCGGGGTGGTGCGCGAGCGCTCCGGCGAACTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ATCACCGCGGTCGACGCCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
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                                                                                                                                                                                                                                                                                                                                                                               121 ATCGGGCCTAGCGCCTTCCTCGCCTTGGGTGTTGTCGACAACAACAACGGCGCACGA
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                                                                                                    Campos-Neto, A.,
                                                                                                                                                                                                                              Length 447;
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                                                                                      1 (bases 1 to 447)
Reed, S.G., Skerky, Y.A.W., Dillon, D.C., Campos-Neto, P. Qedick, T.S. and Twardzik, D.R.
Compounds and methods for diagnosis of tuberculosis Patent: US 6338852-A 4 15-JAN-2002;
                                                                                                                                                                                          1 others
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9
                                                                                                                                                                                                                           Score 394.4; DB 6;
Pred. No. 9.2e-57;
0; Mismatches 1;
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Sequence 4 fisom patent US 6338852.
AR182442
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AR194825
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1. .447
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146 c 149 g
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146 c 149 g
                       AR182442.1 GI:20225649
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Best Local Similarity 99.7%;
Matches 395; Conservative
                                                                           Unclassified.
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Reed.S.G., Skeiky,Y.A.W., Dillon,D.C., Campos-Neto,A., Houghton,R., Vedvick,T.S. and Twardzik,D.R.
Compounds and methods for immunotherapy and diagnosis of tuberculosis
Patent: US 6290969-A 4 18-SEP-2001;
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Pred. No. 9.2e-57;
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Sequence 4 from patent US 6290969.
AR169152 GI:17906927
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Compounds and methods for immunotherapy and diagnosis tuberculosis
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Pred. No. 9.2e-57;
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CORIXA CORPORATION (US)
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Sequence 4 from Patent 1
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AX429596.1 GI:21540845
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Local Similarity 99.7%;
les 395; Conservative
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Vedvick,T.S., Twardzik,D.R., Lodes,M.J. and Hendrickson,R.C.
Compounds and methods for diagnosis of tuberculosis
Patent: US 6458366-A 4 01-0CT-2002;
Location/Qualifiers
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Pred. No. 9.2e-57;
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ANTONIO CAMPOS
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GO1N33/50,G01N33/60,G01N33/569,C12N1/19,C12N1/20,C12N1/21, PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ATCACCGCGGT@GACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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PC C12N15/31,C07K14/35,A61K39/04,A61K48/00,A61K49/00,C12N15/62,
                                                                                                                                                                                                                                                                     08/818112 PI
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                                                                                                                               Reed, S. G., Skelky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R. and Lodes, M.J. Compounds and methods for immunotherapy and diagnosis of Patent: JP 2001501832-A 4 13-FEB-2001;
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Compounds and methods for immunotherapy and diagnosis of
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PN JP 2001$01832-A/4
PD 13-FEB 2001
PP 07-CCT-1997 JP 1998518456
PR 11-OCT-1896 US 08/730510,13-MAR-1997 US
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, PI
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llarity 99.7%; Pred. No. 9.2e-57;
Conservative 0; Mismatches 1;
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
146 c 149 g 77
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Topology: Linear;
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                           BD006445
BD006445.1 GI:18634816
JP 2001501832-A/4.
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                                                                        unidentified unidentified #
               Puberculosis.
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C12N5/10//
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WICHAEL J LODES

C 1207X14/35, CO7X16/12, C1201/68, C12N15/62, G01N33/53 CC

Strandedness: Single;

CC Topology: Linear;

FH Key

I. .447

/ Organism='Unidentified'.
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                                                                                                         1 (bases 1 to 447)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R. and Lodes, M.J.
Compounds and methods for diagnosis of Tuberculosis
Patent: JP 2001500383-A 4 16-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACGGCCGCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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          Compounds and methods for diagnosis of Tuberculosis. BD006325. BD06325.1 GT:18634696 JP 2001500383-A/4.
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PR 11-0CT-1996 US 08/729622,13-MAR-1997 US
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, PI
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/db_xref="taxon:32644"
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PN JP 2001517069-A/4
PN JP 30-AUG-1996 US 08/523436,22-SEP-1995 US 08/553634 PN
JS-MAR-1996 US 08/680574
PI STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS PI RAYMOND HOUGHTON, THOMAS H VEDVICK, DANIEL R TWARDZIK PC CLANI5/31,CO7K14/35,A61K38/16,C12N15/62,G01N33/569,C12Q1/68, PC CLANI5/31,CO7K14/35,A61K38/16,C12N15/11.019)
CC Strandedness: Single;
CC Topology: Linear;
CC Topology: Linear;
CC Topology: Linear;
CC Compounds and methods for immunotherapy and diagnosis of CC
                            27-AUG-2002
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Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.H. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of Patent: JP 2001517069-A 4 02-0cT-2001;
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                                      and methods for immunotherapy and diagnosis
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/organism='Unidentified'
Location/Qualifiers
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99.7%; Pred. No. 9.2e-57;
1ve 0; Mismatches 1;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
                            447 bp
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JP 2001517069-A/4.
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395; Conservative
                                                    tuberculosis.
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RESULT 14
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1 (bases I to 1872)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of
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Patent: US 6290969-A 17 18-SEP-2001;
                                                                                  Sequence 17 from patent US 6290969.
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616 c 604 g
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06-OCT-2000; 2000WO-US27652.
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1 acggccgcgtccgataactt.....tggccgagggaccccggcc 396
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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	39	100.	1068	20	25		
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DE	Nucleotide	e sedneuce	nce encoding	ding	Ral2 protein.		
KW	Ral2; ser	ine pro	tease an	tige	B32A;	cerium	erculosi
K W W	<pre>vaccine; eukaryotic; immunogen; cytokine;</pre>	eukaryo ; cytok	tic; pro ine; gen	kary e; d	gin;	serum antibody;	y, fusion protein;
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                                               Claim 1; Fig 2; 39pp; English.
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Best Local Similarity 100.0
Matches 396; Conservative
            WPI; 2001-266299/27
                 P-PSDB; AA022138
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 kba C-terminal fragment of serine protease antigen MTB32A of Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.

Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.

The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the influences of proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence.
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                                                 Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
immunogen; cytokine; gene; ds.
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Nucleotide sequence encoding Ral2-mammaglobin fusion protein.
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/product= "Ral2-mammaglobin fusion protein"
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Chimeric - Unidentified.
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                                                                                                                                             Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACGCCCCCGCTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 396; DB 23; Length 396; 100.0%; Pred. No. 1.1e-84;
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144 180

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GTCCAACGCGTGGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG 240

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03-OCT-2002 (first entry)

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                                                                                                                                                                                                                     GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCCGCGT 360
                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ral2; serine protease antigen; WTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant nucleic acid molecule encoding fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14
25 ACGCCCCCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                        GTCCAACGCGTGGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                              Nucleotide seguence encoding Ral2-DPPD fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        385 - ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAL40770 standard; DNA; 702 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky Y, Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-266299/27.
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GTCCAACGCGTGGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG 264
                                                   This DNA sequence includes a coding region for a recombinant Mycobacterium tuberculosis bi-antigen fusion protein (see AAY32071), termed Mtb24, composed of the antigens Ral2 and DppD. The DNA is useful for the recombinant production of the fusion protein. Coding sequences for the antigens were modified by PCR in order to facilitate their fusion and subsequent expression of the fusion protein. AAY32059-71) containing at least 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via in vitro assays or intradermal skin tests for detection of anti-M.
                                                                                                        GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New fusion proteins useful for diagnosis, prevention and treatment of tuberculosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis antigen fusion protein Mtb24 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tuberculosis; antigen; fusion protein; Mtb24; Ra12; DPPD; diagnosis; therapy; vaccine; immunogen; ss.
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                                                                                                                                                                                                    361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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98US-0223040.
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30-DEC-1998;
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1 ACGGCCGCGTCCGATAACTTCCAGGTGCTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 60

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1 ACGCCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 60
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SKEIKY Y A.
DILLON D C.
ALDERSON M.
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07-APR-1998;
30-DEC-1998;
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(ALDE/)
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       Mycobacterium.tuberculosis, and a heterologous polynuclectide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cottokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence represents the DNA encoding the Ral2-DPPD fusion protein.
                                                                                                                                                                                                                                                                                                                240
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/note= "No start or stop codon. Xaa= In frame stop codon"
2..702
                                                                                                                                                                                                                                                                       205 GTCCAACGCCTGGTCGGGAGCGCTCCGGCGCGCAAGTCTCGGCATCTCCACCGGCGAGGTG 264
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0
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 C-terminal fragment of serine protease antigen MTB32A of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding antigenic fusion protein Ra12-DPPD (Mtb24).
                                                                                                                                                               Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculostatic; immunogen; vaccine; Ral2-DPPD; Mtb24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - Mycobacterium tuberculosis.
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Matches 396; Conservative
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                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_except= (pos:321..323, aa:Xaa)
/transl_except= (pos:450..452, aa:Xaa)
/transl_except= (pos:450..452, aa:Xaa)
/transl_except= (pos:450..623, aa:Xaa)
/transl_except= (pos:450..623, aa:Xaa)
/note= "No start or stop codon. Xaa= In frame stop codon"
                                                                                                                                                                                                                                                              nucleotide deletion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                          /transl_except= (pos:263..265, aa:xaa)
/transl_except= (pos:353..355, aa:xaa)
/transl_except= (pos:395..397, aa:xaa)
/transl_except= (pos:470..472, aa:xaa)
/transl_except= (pos:701..702, aa:xaa)
/note= "finis codon has an apparent 1 nucl
which alters the reading frame.
xaa= In frame stop codon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aa:Xaa)
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                                                                   stop
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P-PSDB; AAU74600, AAU76541, AAU76542.
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/product- "Mtb24 #2"
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98US-0025197.
98US-0056556.
98US-0223040.
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Matches 396; Conservative
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fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynuclectide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MI5, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, so in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis mature Ra35 (N-terminus of MTB32A; RA35FL) antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; immunity; diagnostic agent; gene therapy; Ra35FLMutSA; mutant; gene; antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
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                                                                                                                                                                                                                                                                                                                                                                            GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
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                                                                                                                                                                                                                                                                                  Ouery Match 100.0%; Score 396; DB 24; Best Local Similarity 100.0%; Pred. No. 1.2e-84; Matches 396; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ra35FLMutSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and
                                                                                                                                                                                                                 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                   ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; immunity; diagnostic agent; gene therapy; Ra35 antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "Ra35 mature antigenic protein" /transl_except= (pos:547..549, aa:Asp) /transl_except= (pos:550..552, aa:Ser)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tuberculosis mature Ra35 antigen encoding
                                                                                                                                                                                                                                                                                                                                                                                                                              ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 420
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/product= "
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P-PSDB; AAE29702.
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Fusion protein; antigen; serological sensitivity; immune response;
tuberculosis; infection; vaccine; MTB32A; Ra32FL; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising MTB39 antigen and MTB32A antigen from um species, useful for eliciting immune response in
                                         Mycobacterium sp. MTB32A (Ra35FL) mature protein encoding cDNA
                                                                                                                                                                            /product= "Ra35 mature protein"
/transl_except= (pos:547..549, aa:Asp)
/transl_except= (pos:550..552, aa:Ser)
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                                                                                                                                     Location/Qualiflers
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                                                                                                                                                                                                                                                                                          20-JUN-2001; 2001WO-US19959.
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01-FEB-2001; 2001US-265737P.
              (first entry)
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/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium species, subject
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                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP
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Best Local Similarity
                                                                                                             Mycobacterium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAE17566
                                                                                                                                                                                                                                    WO200198460-A2
              22-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition
                                                                                                                                                                                                                                                                27-DEC-2001
  The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis Ra35FLMutSA mutant antigenic protein encoding DNA.
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                                                                                                                                                               New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 396; DB 24; Length 1002;
1larity 100.0%; Pred. No. 1.2e-84;
Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1002 BP; 169 A; 331 C; 341 G; 161 T; 0 other;
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                                                                                                                                                                                                                                   Disclosure; Page 80-81; 155pp; English.
                                                                                             Guderian J;
            13-MAR-2002; 2002WO-US08223.
                                      13-MAR-2001; 2001US-275837P.
                                                                                             Skeiky Y, Brannon M,
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Matches 396; Conserva
                                                                                                                       WPI; 2002-759844/82.
                                                                   (CORI-) CORIXA CORP
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with it uberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BGC. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnosis for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the intibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunosens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. WHB32A full anticadarmal skin test. The present sequence is a cona gents of the invention are useful as in vivo diagnostic agents Mycobacterium species MTB32L) mature protein.
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100.0%; Pred. No. 1.2e-84;
11ve 0; Mismatches 0;
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AAD28336 standard; cDNA; 1002

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                                                                                                                                                                                      GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
                                                                                                                                   241 ATCACCGCGGTCGACGCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
                                                                                                                                                              897
The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nuclectides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with tuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention are
                                    GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                           ATCGGGCCTACCGCCTTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein; antigen; serological sensitivity; immune response;
tuberculosis; infection; vaccine; Ra32FLMutSA; mutant; mutein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a
                                                                                                                                                                                                                                        "Ra35FLMutSA protein"
                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium species Ra35FLMutSA mutant cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 67; Page 96-97; 136pp; English.
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4..996
/*tag= a
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                                                                                                                                                                                                                                                                                                                                       AAD28337 standard; cDNA; 1002
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01-FEB-2001; 2001US-265737P.
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useful for eliciting an immune response in a mammal, e.g., human, immunised with BGG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. WIB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a cDNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG
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                                                                                                                                                                                                                                                                                                                                 4ycobacterium species Ra32FL mature protein mutant, Ra32FLMutSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1002 BP; 169 A; 331 C; 341 G; 161 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 396; DB 24;
100.0%; Pred. No. 1.2e-84;
iive 0; Mismatches 0;
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97FR-0010404
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Matches 396; Conserv
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985 ATCACCGGGTCGACGCCCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 1044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
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                                                                                                                                                                                                                                                                              Sequences AAX34001-X34252 represent nucleic acids encoding secreted proteins from various Mycobacterium species microorganisms. The nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
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                                                                                                                                                                                                  Mycobacterial DNA vectors containing reporter constructs · identifying coding or promoter sequences involved in infection-associated protein expression
                                                                                                                                                                                                                                                                                                                                                                        Sequence 1143 BP; 189 A; 373 C; 395 G; 186 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence encoding Ral2-WT1 fusion protein.
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                                                                                                                      Pelicic V,
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                                                    97FR-0011325
                                                                97FR-0010404
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Best Local Similarity 100.(
Matches 396; Conservative
                                                                                           (INSP ) INST PASTEUR
                                                                                                                      Lim EM,
                                                                                                                                                          WPI; 1999-181045/15.
P-PSDB; AAY04830.
                                                                14-AUG-1997;
                          14-AUG-1998;
25-FEB-1999.
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                                                   11-SEP-1997
                                                                                                                                    Guigueno A;
                                                                                                                  В,
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                          Salmoniere Y;
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                                                                                                                                                                                                 proteins from various Mycobacterium species microorganisms. The nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
                                                                                                                                                                                   Sequences AAX34001-X34252 represent nucleic acids encoding secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection; ss.
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                                                                                                                                                                                                                                                                                                       100.0%; Score 396; DB 20; Length 1068; 100.0%; Pred. No. 1.2e-84;
                                                                                                         constructs -
                          Goguet de la
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                               · Sequence 1068 BP; 169 A; 352 C; 375 G; 172 T; 0 other;
                                                                                                     Mycobacterial DNA vectors containing reporter construidentifying coding or promoter sequences involved in infection-associated protein expression
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                         Pelicic V, Portnoi D,
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                           22; F1g 50D; 309pp; French
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Matches 396; Conservative
(INSP ) INST PASTEUR
                         Lim EM,
                                                              WPI; 1999-181045/15.
P-PSDB; AAY05000.
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                                      Guigueno A;
                         Gicquel B,
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                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                           Claim
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GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGGGGCACGGT

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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 to MacCaterinal fragment of serine protease antigen WTB32A of Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.

Mycobacterium tuberculosis, and a heterologous polynucleotide sequence.

The recombinant fusion nucleic acids and polypeptides are useful for customy atable and high yield expression of fusion polypeptides of both cukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses.

The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence.
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Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
immunogen; cytokine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACGCCCCCCTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                            Location/Qualifiers
4..1740
/*tag= a
/product= "Ral2-WT1 fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 4; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-OCT-2000; 2000WO-US27652
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                                                                                                                                 Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky Y, Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-266299/27.
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Best Local Si
Matches 396;
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fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are used in methods for elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is a DNA encoding WIB72F fusion protein. This fusion protein comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a recombinant nucleic acid molecule encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis
                                                                                                                                                                                   immunity; diagnostic agent; gene therapy; TbH9; antigen;
                                                                                                                                             Mycobacterium sp. MTB72FMutSA fusion protein encoding DNA
                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..239 /
/*tag a
/product = "MTB72FMutSA fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2190 BP; 340 A; 697 C; 797 G; 356 T; 0 other;
                                                                                                                                                                                                     Ra35MutSA; Ra12; MTB72MutSA; chimeric; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 92-93; 155pp; English.
                                                                                                                                                                                                                                       Chimeric - Mycobacterium sp.
Chimeric - Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein from Mycobacterium sp.
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                                  AAD47084 standard; DNA; 2190
                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-MAR-2002; 2002WO-US08223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2001; 2001US-275837P
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Skeiky Y, Brannon M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-759844/82.
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RESULT 1
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Alderson M;

us-09-684-215a-3.rng

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(CORI-) CORIXA CORP
                      Skeiky Y, Reed S,
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                                   ATCGGGCCTACCGCCTTCCTCGGCTTTGTCGACAACAACGGCAACGGCGCACGA
                                                                                                                GTCCAACGCGTGGTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                           ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
                                                                                                                                                    GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT
                            ACGCCCCCCCCATCCAGCTCTCCAGCTGTCCCAGGGCAGGGATTCGCCATTCCGATC
               Gaps
                                                                                                                                                                                                                                                                                                           Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB72FMutSA; Ral2-TbH9-Ra35MutSA;
               ö
                                                                                                                                                                                                                                                                                              Mycobacterium species MTB72FMutSA fusion protein encoding DNA.
Length 2190;
               Indels
                                                                                                                                                                                                                                                                                                                                                                          'product" "MTB72FMutSA fusion protein"
                                                                                                                                                                                                          ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 417
                                                                                                                                                                                                   ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
100.0%; Score 396; DB 24; 100.0%; Pred. No. 1.3e-84;
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/note= "Ral2 DNA fragment"
424..1596
/*tag= "TbH9FL DNA fragment"
              0; Mismatches
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/*tag= d
/note= "Ra35 DNA fragment"
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1..2190
/*tag= a
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                                                                                                                                                                                                                                                    AAD28343 standard; DNA; 2190
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01-FEB-2001; 2001US-265737P.
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                                                                                                                                                                                                                                                                                (first entry)
              Conservative
        Similarity
                                                                                                                                                                                                                                                                                                                         mutant; mutein; ds
                                                                                                                                                                                                                                                                                                                                       Mycobacterium sp.
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              396;
Query Match
Best Local S:
Matches 396
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the Mycobacterium species antigates, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual w. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with increase the serological sensitivity of sera from individuals infected with treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immunogens in a non-human animal. Sequences of the invention are also used as vaccines. WTB32A fusion proteins of the invention are also used as vaccines. WTB32A fusion proteins of the invention are also used as vaccines. WTB32A fusion proteins of the invention are useful as in vivo diagnostic agents for intradermal skin test. The present sequence is a DNA encoding manner.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 ACGCCCCCCTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCAACGCGTGGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACGCCCCCCTCCCATTAACTTCCAGCTGTCCCAGGCTGGCCAGGGATTCCCCATTCCCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                         present invention relates to fusion proteins containing at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2190 BP; 340 A; 697 C; 797 G; 356.T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 396; DB 24;
; Pred. No. 1.3e-84;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                      Claim 81; Page 108-109; 136pp; English.
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 396; Conservative
                                                                                                                   Mycobacterium species,
subject -
WPI; 2002-147798/19.
P-PSDB; AAE17573.
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                                                                                                                                                                                                                                                                  Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
Immunogen; cytokine; gene; ds.
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                                                                                                                                                                                                      Nucleotide sequence encoding Ral2-H9-32A fusion protein.
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/product- "Ral2-H9-32A fusion protein"
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                         AAL40773 standard; DNA; 2191 BP.
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P-PSDB; AA022142.
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                  GTCCAACGCGTGGTCGGCGCAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
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396
1 acggccgcgtccgataactt......tggccgagggaccccggcc 396
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Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli		4	4	4	17,	17,	17,	17,	1862		353,		351,	351,	Sequence 348, App	348,	332,	332,	188,	188,	188,		352,	226
	Desc	Sec	Š	Se	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Sec	Č
SUMMAKIES	ID	US-09-223-040-1	US-09-103-840A-2	US-09-103-840A-1	US-08-818-11.2-4	US-08-818-111-4	US-09-056-556-4	US-09-072-596-4	US-08-818-112-17	US-08-818-111-17	US-09-056-556-17	US-09-072-596-17	US-09-736-457-1862	US-09-643-597-353	US-09-606-421B-353	US-09-736-457-1861	US-09-643-597-351	US-09-606-421B-351	US-09-620-412C-348	US-09-598-419-348	US-09-620-412C-332	US-09-598-419-332	US-09-556-877-188	US-09-620-412C-188	US-09-598-419-188	US-09-620-412C-352	US-09-598-419-352	366-0617-063-00-011
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1758 4 1860 4 1860 4 1860 4 1860 4 1941 1941 1941 1941 1941 1965 4 2052 4 2076 4 2103 4 4 2148 4 2148 4 2148 6 4		1.040-1  1.0. Application US/09223040  No. 6544522  INFORMATION: ANT: Skeiky, Yasir Ant: Skeiky, Yasir Ant: Corixa Corporation OF INVENTION: Fusion Protei OF INVENTION: and Their Use EFFERNCE: 014058-009010US IT FILING DATE: 1998-12-30  NE: PALCATION NUMBER: US/09/ IT FILING DATE: 1998-12-30  NE: PALCATION OF: 2.1  NNO 1  HH: 2287  DNA ILISM: Artificial Sequence RE: INFORMATION: Description of ILISM: Artificial Sequence RE: INFORMATION: Description of INFORMATION: protein Ra12-T KEY: modified_base ION: (30) INNO (31) INNO (32) INNO (32) INNO (32) INNO (33) INNO (33) INNO (34) INNO (34) INNO (35) INN	100.0%; 100.0%; ive
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LENGTH: 4411529
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                                                                                                                                  GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
                                                                                                                                              various positions throughout the sequence \mathsf{t}, \mathsf{c} or \mathsf{g}
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FASER, Claire M.
APPLICANT: FASER, Claire M.
APPLICANT: PRASER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-220007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
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                                                                                                                                                                                                  ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION UNMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
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ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
                                                                                                                                            ; Sequence 1, Application US/09103840A; Patent No. 6294328
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Patent No. 6290969
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Matches 396; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCCAACGCGTGGTCGGGAGCGCTCCGGCGCAAGTCTCGGCATCTCCACCGGCGACGTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 ACGCCCCCGTCCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 447;
   COMPOUNDS AND METHODS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR 1997
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-631
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                        E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         371 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 394.4; DB 3,
Pred. No. 3.8e-91;
0; Mismatches 1,
                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.68;
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 447 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 99.7
Matches 395; Conservative
TITLE OF INVENTION: CONTITLE OF INVENTION: ANI NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                        Washington
                                                                                                                                   ZIP: 98104-7092
                                                                                        CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                      USA
                                                            ADDRESSEE:
                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 447;
                  APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
NUMBER OF SEQUENCES: 148
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY,AGENT INFORMATION:
NAME: Maki, David J.
REFERRENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                              3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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Pred. No. 3.8e-91;
0; Mismatches 1;
Skeiky, Yasir A.W.
Dillon, Davin C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 99.7
Matches 395; Conservative
                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
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                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                              ADDRESSEE:
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RESULT

Sequence 4, Application US/08818111 Patent No. 6338852 GENERAL INFORMATION:

US-08-818-111-4

Reed, Steven G.

APPLICANT:

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TUBERCULOSIS
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                                                                                                                                APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardisk, Thomas S.
APPLICANT: Twardisk, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: APPLICANT: TWARDISK OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                               2: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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Best Local Similarity 199.7%; Pred. No. 3.8e-91;
Matches 395; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET MUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) [622-4900
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: FloRBY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
                                                                            Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonia
Houghtom, Raymond
Vedvick, Thomas S.
                    Sequence 4, Application US/09072596 Patent No. 6458366 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (206) 622-4
TELEFAX: (206) 662-603
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 447 base pair
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                               STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-072-596-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCCAACGCGTGGTCGGGGGCCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/09/056,556 FILING DATE: 07-APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.6%; Score 394.4;
99.7%; Pred. No. 3.8e
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION UNBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPEX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 4, Application US/09056556
Patent No. 6350456
                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.7
Matches 395; Conservative
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                      STREET: 6300 Colum
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US:09-056-556-4
                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98104-7092
                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
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g à g à 셤 à g ò g ò GGGCATCATCCCGGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACA 

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241 ATCACCGCGGTCGACGCCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 300
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                    301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardaik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
WUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                          ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6300 Columbia Center, 701 Fifth Avenue
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Pred. No. 3.1e-90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Fatentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              Sequence 17, Application US/08818111
Patent No. 6338652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEED and BERRY LLP
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 98.8%;
Best Local Similarity 99.2%;
Matches 393; Conservative
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STATE: Washington
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US-08-818-111-17
                                                                                                                                                                                                                                                 US-08-818-111-17
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CURRENT APPLICATION DATA:
ELICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
                                                 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 391.2; DB 3;
Pred. No. 3.1e-90;
0; Mismatches 3;
                                   361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METITLE OF INVENTION: AND DIAGNOSIS OF NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Rainana.
                                                                                                                                  US-08-818-112-17
; Sequence 17, Application US/08818112
; Patent No. 6290969
                                                                                                                                                                                                         APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 17:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 98.8%;
Best Local Similarity 99.2%;
Matches 393; Conservative
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LENGTH: 1872 base pairs
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STATE: Washington
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US-08-818-112-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
311
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Db   878   ATCGGGCCTAGCTTCGTCGGCTGGCGAACGGCAACGGCGACGA   937     Oy	RESULT 11 US-09-072-596-17, R Sequence 17, R PRICANT: APPLICANT: A	1872 base pairs nucleic actd EDNESS: single 37: linear	Ouery Match  Best Local Similarity 99.2%; Pred. No. 3.1e-90;  Bast Local Similarity 99.2%; Pred. No. 3.1e-90;  Matches 393; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Qy 1 ACGCCGCGTCCGATCCAGCTCTCCCAGGGTGGCCAGGGATTCCCCATTCCGATC 60
Qy         181 GTCCAACGCGTGGTCGGGAGCTCCGGCGAAGTCTCCGCCATCTCCACCGGCGACGTG         240           Db         938 GTCCAACGCGTGGTCGGCGCCACCGGCGACGTCCGGCGACGTG         997           Qy         241 ATCACCGCGTCGACGCGCTCCGGCGCACCGCGATGCCGGACGCGTTAAC         300           Db         998 ATCACCGCGGTCGACGCGCTCCGATCACCGCCACCGCGATGCCGCTTAAC         1057           Qy         301 GGCCATCCCGGTCCCGATCACTCGCCCACCGCGCGCGCGC	RESULT NO. 6354676  Sequence 17, APPLICATION US/09056556  Patent No. 6354656  APPLICANT: Steaky, Yasir A.W. APPLICANT: Steaky, Yasir A.W. APPLICANT: Dillon, Davin C. APPLICANT: Steaky, Yasir A.W. APPLICANT: Steaky Yasir A.W. APPLICANT: Steaky A.W. APPLICANT: Steak A.W. APPLICANT: Steak A.W. APPLICANT: COMPURES: Steak A.W. APPLICANT: COMPURES: Steak A.W. APPLICANT: COMPURES: Proper Steak A.W. APPLICANT: COMPURES: Proper Steak A.W. APPLICANT: Steak A.W. APPLICANT: NO. APPLICANT: APPL	SIMITATILY 59.2%; 3; Conservative 0 ACGCCGCGTCCGATAACTT	Oy         61 GGGCAGGCGATGGCGGGCCAGATCGGATCGGGTGGGGGTCACCCACGTTCAT 120           1

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241 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGCGGTGGCGGACGCGCTTAAC 300
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APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aljun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478015
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT APPLICATION DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1861
LENGTH: 945
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 89.4%; Score 354; DB 4; Length 945; Best Local Similarity 95.7%; Pred. No. 7e-81; Matches 379; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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Job time : 87 secs
    Carter, Darrick
                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-09-736-457-1861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                       APPLICANT: Rails, Michael D.
APPLICANT: Rails, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Banger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Wang, Aljun
APPLICANT: Wasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: ADD DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT APPLICATION NUMBER: US/09.606,421B
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 354; DB 4; Length 900;
Pred. No. 6.9e-81;
0; Mismatches 5; Indels
370 ACAGGGAACGIGACATIGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 405
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                                                                               US-09-606-421B-353

Sequence 353, Application US/09606421B

; Patent No. 65131315

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1861, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
                                                                                                                                                                   APPLICANT: Wang, Tongtong
APPLICANT: Fan, Ligun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
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95.7%;
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APPLICANT: Bangur, Chaitanya
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 95.7
Matches 379; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-606-421B-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-736-457-1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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120 129

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Gaps

12;

81

240 249 309

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

September 5, 2003, 07:20:04; Search time 1535 Seconds Run on:

(without alignments) 593.349 Million cell updates/sec

396 1 acygccgcgtccgataactt.....tggccgagggacccccggcc 396 US-09-684-215A-3 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapoxt 1.0 Scoring table:

Total number of hits satisfying chosen parameters: 1537136 seqs, 1149988732 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

3074272

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published\_Applications\_NA:\*

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/cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Sequence 27, Appl	Sequence 27, Appl	Sequence 15, Appl	Sequence 1, Appli	Sequence 1, Appli		Sequence 4, Appli	Sequence 17, Appl	Sequence 17, Appl	Sequence 822, App	Sequence 822, App	Sequence 822, App	Sequence 822, App	Sequence 822, App	Sequence 822, App	Sequence 822, App
ΙD	US-09-287-849-27	US-10-359-460-27	US-09-712-363-15	US-09-287-849-1	US-10-359-460-1	US-10-084-843-4	US-10-193-002-4	US-10-084-843-17	US-10-193-002-17	US-09-759-143-822	US-09-780-669-822	US-09-822-827-822	US-09-895-793-822	US-09-895-814-822	US-10-144-678A-822	US-10-012-896-822
DB	9	12	10	6	12	12	12	12	12	6	6	6	10	12	17	13
Length	702	702	1068	2287	2287	447	447	1872	1872	675	675	675	675	675	675	675
Query Match	100.0	100.0	100.0	100.0	100.0	99.6	9.66	98.8	98.8	89.4	89.4	89.4	89.4	89.4	89.4	89.4
Score	396	396	396	396	396	394.4	394.4	391.2	391.2	354	354	354	354	354	354	354
Result No.	1	7	e	4	2	9	7	80	6	10	11	12	13	14	15	16
	Query Score Match Length DB ID	Query Score March Length DB ID 396 100.0 702 9 US-09-287-849-27	Query         Query         Description           Score Match Length DB ID         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0         100.0     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9 US-09-287-849-27 Sequence 27, 396 100.0 702 1 US-10-359-460-27 Sequence 27, 396 100.0 1068 10 US-09-287-353-15 Sequence 17, 396 100.0 2287 9 US-09-287-849-1 Sequence 1, 394 100.0 2287 1 US-10-359-460-1 Sequence 1, 394 4 99.6 447 12 US-10-084-843-4 Sequence 1,	Score Match Length DB ID Description  396 100.0 702 9 US-09-287-849-27 Sequence 27, 396 100.0 702 12 US-10-359-460-27 Sequence 27, 396 100.0 1068 10 US-09-712-363-15 Sequence 12, 396 100.0 2287 12 US-10-359-460-1 Sequence 1, 394.4 99.6 447 12 US-10-084-843-4 Sequence 4, 394.4 99.6 447 12 US-10-193-002-4 Sequence 4, 394.4 99.6 447 12 US-10-193-002-4 Sequence 4,	Score Match Length DB ID Description  396 100.0 702 9 US-09-287-849-27 Sequence 27, 396 100.0 702 12 US-10-359-460-27 Sequence 27, 396 100.0 2287 9 US-09-287-849-1 Sequence 1, 396 100.0 2287 12 US-10-359-460-1 Sequence 1, 394.4 99.6 447 12 US-10-084-843-4 Sequence 4, 394.2 99.6 447 12 US-10-084-843-4 Sequence 4, 394.2 99.6 100.0 288 1872 US-10-084-843-4 Sequence 4, 394.2 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US-10-084-843-17 Sequence 17, 391.2 98.8 1872 12 US-10-084-843-17 Sequence 17, 391.2 98.8 1872 12 US-10-084-843-17 Sequence 17, 391.2 98.8 1872 12 US-10-193-002-17 Sequence 17, 391.2 98.8 US-08-08-08-08-08-08-08-08-08-08-08-08-08-	Score Match Length DB ID  396 100.0 702 9 US-09-287-849-27 Sequence 27, 396 100.0 702 1 US-10-359-460-27 Sequence 27, 396 100.0 2287 12 US-10-359-460-1 Sequence 1, 396 100.0 2287 12 US-10-359-460-1 Sequence 1, 394.4 99.6 447 12 US-10-389-460-1 Sequence 1, 394.4 99.6 447 12 US-10-193-002-4 Sequence 4, 394.2 98.8 1872 12 US-10-193-002-4 Sequence 1, 394.3 98.8 1872 12 US-10-193-002-1 Sequence 1, 394.8 98.8 1872 12 US-10-193-002-1 Sequence 1, 354.8 94.8 675 9 US-09-759-143-822 Sequence 1, 394.8 98.8 98.8 98.8 98.8 98.8 98.8 98.8	Score Match Length DB ID  396 100.0 702 9 US-09-287-849-27 Sequence 27, 396 100.0 702 12 US-10-359-460-27 Sequence 27, 396 100.0 2287 12 US-10-359-460-1 Sequence 17, 396 100.0 2287 12 US-10-359-460-1 Sequence 13, 394.4 99.6 447 12 US-10-359-460-1 Sequence 1, 394.4 99.6 447 12 US-10-084-843-4 Sequence 1, 394.2 98.8 1872 12 US-10-193-002-4 Sequence 1, 391.2 98.8 1872 12 US-10-193-002-17 Sequence 1, 391.2 98.8 1872 12 US-10-193-002-17 Sequence 1, 391.3 98.4 675 9 US-09-759-143-822 Sequence 822 Sequence 822	Score Match Length DB ID Description  396 100.0 702 9 US-09-287-849-27 Sequence 27, 396 100.0 1068 10 US-09-123-363-15 Sequence 17, 396 100.0 2287 12 US-10-359-460-1 Sequence 17, 396 100.0 2287 12 US-10-359-460-1 Sequence 1, 394.4 99.6 447 12 US-10-384-849-1 Sequence 1, 394.2 99.6 447 12 US-10-384-843-4 Sequence 1, 391.2 98.8 1872 12 US-10-193-002-4 Sequence 17, 391.2 98.8 1872 12 US-10-193-002-17 Sequence 17, 391.2 98.8 1872 12 US-10-193-002-17 Sequence 17, 391.2 98.8 1872 12 US-10-193-002-17 Sequence 17, 391.2 98.8 US-09-759-143-822 Sequence 822 354 89.4 675 9 US-09-789-1822 Sequence 822 Sequence 822 354 89.4 675 9 US-09-789-1822 Sequence 822 Sequence 822 354 89.4 675 9 US-09-789-1822 Sequence 822 SEQUENCE 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822,	Score Match Length DB ID  396 100.0 702 9 US-09-287-849-27 Sequence 27, 396 100.0 702 12 US-10-359-460-27 Sequence 27, 396 100.0 2287 12 US-10-359-460-1 Sequence 17, 394.4 99.6 447 12 US-10-359-460-1 Sequence 1, 394.4 99.6 447 12 US-10-359-460-1 Sequence 1, 394.4 99.6 447 12 US-10-359-460-1 Sequence 1, 394.2 99.8 1872 12 US-10-139-002-4 Sequence 1, 391.2 98.8 1872 12 US-10-139-002-4 Sequence 1, 391.2 98.8 1872 12 US-10-139-002-17 Sequence 1, 391.2 98.8 1872 12 US-10-193-002-17 Sequence 822 354 89.4 675 9 US-09-780-669-822 Sequence 822 354 89.4 675 10 US-09-895-73-822 Sequence 823 354 89.4 675 10 US-09-895-814-822 Sequence 823 354 89.4 675 10 US-09-895-814-882

Sequence 1862, Ap Sequence 1862, Ap Sequence 1862, Ap Sequence 353, App Sequence 353, App Sequence 353, App Sequence 344, App Sequence 834, App Sequence 834, App Sequence 834, App Sequence 834, App Sequence 1861, App Sequence 1861, App Sequence 1861, App Sequence 1861, App Sequence 314, App Sequence 3184, App Sequenc	
10 US-09-736-457-1862 10 US-09-902-911-1862 US-09-902-911-1862 US-09-735-705-353 US-09-735-705-353 US-09-735-706-353 US-09-735-706-353 US-09-735-716A-353 US-09-759-1484 US-09-759-1484 US-09-822-827-834 US-09-822-827-834 US-09-822-827-834 US-09-829-834 US-09-829-834 US-09-829-834 US-09-829-834 US-09-829-834 US-09-902-941-1861 US-09-902-941-1861 US-09-902-941-1861 US-09-902-941-1861 US-09-902-941-1861 US-09-902-941-1861 US-09-902-941-1861 US-09-902-941-1861 US-09-902-941-1861 US-09-902-941-1861 US-09-902-941-1861 US-09-903-941-1861 US-09-903-941-1861 US-09-903-941-1861 US-09-903-941-1861 US-09-903-941-1861 US-09-903-941-1861 US-09-903-903-1084 US-09-903-903-1084	200
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## ALIGNMENTS

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APPLICANT: Campos-Natco, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: And Their Uses
TITLE OF INVENTION: And Their Uses
FILE REFERENCE: 014058-0090200S
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-00-01
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOSTWARE: PATENTIN VOIL 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(693) OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence:bi-fusion OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading OTHER INFORMATION: frame 1
Sequence 27, Application US/09287849 Patent No. US20020009459A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                              APPLICANT: Reed, Steven G.
APPLICANT: Skeixy, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
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Sequence 15, Application US/09712363 Patent No. US20020164588A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (3)..(701)
; OTHER INFORMATION: reading frame
US-10-359-460-27
                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (2)..(700)
OTHER INFORMATION: reading frame
                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (1)
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APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
ITILE OF INVENTION: Endson Protiens of Mycobacterium tuberculosis Antigens
ITILE OF INVENTION: and Their Uses
FILE REPERENCE: 014058-0092003
FURENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 1090-02-05
FRIOR APPLICATION NUMBER: US/08/818,112
FRIOR FILING DATE: 1997-03-13
FRIOR FILING DATE: 1997-03-13
FRIOR PRIOR APPLICATION NUMBER: US 08/942,578
FRIOR APPLICATION NUMBER: US 09/025,197
FRIOR APPLICATION NUMBER: US 09/025,197
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DATE: 1998-04-17
FRIOR FILING DATE: 1998-04-07
FRIOR FILING DAT
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                                                                                                                                                                                                                                                            Length 702;
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                                                                                                                                                                                                                                                      100.0%; Score 396; DB 9; L
100.0%; Pred. No. 7.1e-104;
tive 0; Mismatches 0;
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                                                                                                                              ; LOCATION: (3)..(701); OTHER INFORMATION: reading frame 3 US-09-287-849-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 27, Application US/10359460 Publication No. US20030147911A1 GENERAL INFORMATION:
                                                                                 OTHER INFORMATION: reading frame
OTHER INFORMATION: reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 396; Conservative
                                                   ..(700)
                                                                                                            NAME/KEY: CDS
LOCATION: (3).
                        NAME/KEY: CDS
LOCATION: (2)
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APPLICANT: Elsenberg, David
APPLICANT: Elsenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Rotstein, Sergio H.
TITLE OF INVENTION: DIFFERINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE REFERENCE: 07419-032001
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: PCT/US00/02246
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-01
PRIOR PLICATION NUMBER: 60/117,844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 ACGCCCCCCCCATAACTTCCAGCTGTCCCAGGGTGGCCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                               LOCATION: (1)..(693)
OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
OTHER INFORMATION: reading frame 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . o
OTHER INFORMATION: Description of Artificial Sequence:b1-fusion OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading OTHER INFORMATION: frame 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Pred. No. 7.1e-104;
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Best Local Similarity 100.0%; Pred. No. 7.1
Matches 396; Conservative 0; Mismatches
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US-10-359-460-1
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Best Local S
Matches 396
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APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1068
                                       PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
PRIOR PELLATION NUMBER: 60/134,093
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/134,092
PRIOR FILING DATE: 1999-05-14
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                TYPE: DNA COBACTERIUM TUBERCULOSIS US-09-712-363-15
           APPLICATION NUMBER: 60/118,206 FILING DATE: 1999-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09287849
Patent No. US20020009459A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yaair A.W.
APPLICANT: Dillon, Davin C.
FILING DATE: 1999-01-29
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Best Local S:
Matches 396,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:tr1-fusion OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: fusion)
NAME/KEY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: CDS
LOCATION: (42)...(2231)
NAME/KEY: modified_base
LOCATION: (42)...(2231)
NAME/KEY: modified_base
LOCATION: (42)...(2231)
NAME/KEY: modified_base
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PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR PPLICATION NUMBER: US 09/223,040
PRIOR PILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SSOFWARE: PATENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 2287
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , LUCATION: (2270); OTHER INFORMATION: n = g, a, c
US-09-287-849-1
                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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396; Conservative
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121 ATCGGCCTACECCTTCCTCGCCTTGGGTGTTGTCGACAACAACGCCAACGGCGCACGA 180
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                                                                                                                                                                                                                                                                                                                               Skelky, Yasir A.W.
Dilleh, Davin C.
Camped-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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99.6%; Score 394.4; DB 12; Length 447;
Best Local Similarity 99.7%; Pred. No. 2e-103;
Matches 395; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: 18M PC Compatible
COMPUTER: 18M PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ratentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 55-Feb-2002
CLASSIFICATION: <unknown>
361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFRUME. N-7
INFORMATION FOR SEG 1D NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447' base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206) 622-4900
206) 682-6031
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                                                                                                                                                                                                       Sequence 4, Application US/10084843
Publication No. US20030143243A1
GENERAL INFORMATION:
APPLICANT: Reed Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEOUENCES:
                                                                                                                                                 RESULT 6
US-10-084-843-4
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         ##PILLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
##FILLE OF INVENTION: and Their Uses
#FILE REFERENCE: 014058-00902005
#FILE REFERENCE: 014058-00902005
#CURRENT APPLICATION NUMBER: US/10/359,460
#CURRENT APPLICATION NUMBER: US/09/287,849
#RIOR PRIOR APPLICATION NUMBER: US/09/287,849
#RIOR FILING DATE: 1999-04-07
#PRIOR FILING DATE: 1999-04-07
#PRIOR PILING DATE: 1997-03-13
#PRIOR PILING DATE: 1997-00-01
#PRIOR PILING DATE: 1997-00-01
#PRIOR PILING DATE: 1997-10-01
#PRIOR PILING DATE: 1998-02-18
#PRIOR FILING DATE: 1998-02-30
#PRIOR FILING DATE: 1998-12-30
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301 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (2270)
; OTHER INFORMATION: n = g, a, c or t
US-10-359-460-1
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OTHER INFORMATION: n = g, a, c or
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OTHER INFORMATION: n = g, a, c or
   Corixa Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: NAME/KEY: modified_base
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                      11 ACGCCCCCTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                            181 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                                                                                      251 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIF: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: SOO COlumbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17; Application US/10084843 Publication No. US20030143243A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
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Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
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GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGAAGTCTCGGCATCTCCACCGGCGACGTG 240
                                                                                                  GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGT 360
                                       GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTG
                                                                              ATCACCGCGGTCGACGCCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC
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Dillon, Davin C.
Campos Neto, Antonia
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.6%; Score 394.4; DB 12;
99.7%; Pred. No. 2e-103;
11ve 0; Mismatches 1;
                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10193002
Publication No. US20030135026A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCES: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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Best Local Similarity 99.7
Matches 395; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF
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181
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938 GTCCAACGCGTGGTCGGAAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTG 997
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                                                                                                                                                                                                                                                                                                                                                   Score 391.2; DB 12
Pred. No. 1.7e-102;
                                                                                   NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-WAY-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 822, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
                                                                                                                                                                        TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                           LENGTH: 1872 base pairs
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Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                   98.8%;
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
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Dillon, Davin C.
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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US-09-759-143-822
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ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                      Score 391.2; DB 12;
Pred. No. 1.7e-102;
0; Mismatches 3;
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APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND ME
                                                                 TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
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Publication No. US20030135026A1
GENERAL INFORMATION:
SAPPLICANT: Reed, Steven G.
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Dillon, Davin C.
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                LENGTH: 1872 base pai
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
                                                                                                                                    Query Match 98.8%;
Best Local Similarity 99.2%;
Matches 393; Conservative
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 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: 05/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121:534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 7.1e-92;
0; Mismatches 5;
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Pred. No. 7.1e-92;
0; Mismatches 5
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Best Local Similarity 95.7
Matches 379; Conservative
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US-09-780-669-822
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LENGTH: 675
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Best Local S:
Matches 3799
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Pred. No. 7.1e-92;
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION UNMBER: US/09/759,143
CURRENT APPLICATION UNMBER: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Houghton, Raymond L.
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95.7%;
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Vedvick, Thomas S.
Carter, Darrick
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Hepler, William
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Best Local Similarity 95.7
Matches 379; Conservative
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; ORGANISM: Homo sapiens
US-09-759-143-822
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US-09-780-669-822
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                                                                        121 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGA
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Pred. No. 7.1e-92;
0; Mismatches 5;
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APPLICANT: Foy, Teresa
APPLICANT: Enanger: Gary R
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSIATE CANCER FULE REFERENCE: 210121.427026
FURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILLNG DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
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Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020193296A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Alang, Yuqiu
APPLICANT: Kalos, Michael D.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Best Local Similarity 95.7%;
Matches 379; Conservative (
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Hepler, William T.
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Stolk, John A.
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US-09-895-814-822
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APPLICANT:
APPLICANT:
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LENGTH: 67
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APPLICANT:
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APPLICANT:
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APPLICANT: AL, Jiangenun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Stale, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Winals de Bassols, Carlota
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Panger, William T.
APPLICANT: COMPOSITION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/895,793
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Pred. No. 7.1e-92;
0; Mismatches 5;
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 822, Application US/09895793 Publication No. US20020192763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Hallocker, Susan L.
APPLICANT: Ralos, Michael D.
APPLICANT: Rater Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Day, Craig H.
APPLICANT: Carter, Day, Craig H.
APPLICANT: Li, Samuel X.
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Best Local Similarity 95.7%;
Matches 379; Conservative
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US-09-895-793-822
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US-09-895-793-822
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LENGTH: 675
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Hepler, William T.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Winals y de Bassols, Carlota
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C3B
CURRENT APPLICATION NUMBER: US/10/144,678A
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Pred. No. 7.1e-92;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 822, Application US/10144678A Publication No. US20030157089A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Best Local Similarity 95.7%;
Matches 379; Conservative
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; ORGANISM: Homo sapiens
US-10-144-678A-822
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81
                                                    22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC
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                                   GGGCAGGCGATGGCGATCGCGGGCCAGATCCGATCGGGTGGGGGGTCACCCCACCGTTCAT
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Title: US-09-684-215A-3 Perfect score: 396	v		. C. a	111.4	538		BE215641	
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Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	o .		. 4 4	11.3	1201 496	13	BX360624 BJ307565	
Searched: 22781392 seqs, 12152238056 residues	υ υ			11.2	590		BH190076 BH189840	
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	A	AUTHORS	Silba	q, F. S.,	Cho, S	, z.	Silbaq, F.S., Cho, S.N., Cole, S.T.	
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	3	1110	that	is isol	logous	to t	Characterization of a 54-Kilouary that is isologous to the immunode Wycobacterium paratuberculosis	īσ
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			core Match Length DB ID	289	,	603	925	925	
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			Score	65.2		55.6	50.4	49.6	
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RESULT 1 U82114 LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE	UB2114 ordered cosmid library Mycobacterium leprae genomic clone UB2114 ordered cosmid library Mycobacterium leprae genomic clone UB2114 .1 GI:3647212 GSS. Mycobacterium leprae la Corynebacterium leprae Johnses 1 to 289).  I (bases 1 to 289).  Silbaq.F.S., Cho,S.N., Cole,S.T. and Brennan, P.J.  Silbaq.F.S., Cho,S.N., Cole,S.T. and Brennan, P.J.  Silbacterization of a 34-kilodalton protein of Mycobacterium leprae that is isologous to the immunodominant 34-kilodalton antigen of Mycobacterium paratuberculosis  Infect. Immun. 66 (11), 5576-5579 (1998)
PUBMED COMMENT	9784577 Contact: Silbaq FS Microbiology Colorado State University Fort Collins, CO 80523, USA Fort Collins, CO 80523, USA Fort Collins, CO 80528, USA for Collins, CO 80529, USA for Collins, CO 80529, USA for Collins, CO 80529, USA for Collins, CO 80539, USA for Co

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Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A., Goicoechea,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
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BJ_Ba0002I08r B. japonicum BAC library Bradyrhizobium japonicum
genomic, genomic, survey sequence.
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Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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/lab_host="E. coli"
/clone_lib="B. japonicum BAC library"
/note="Vector: pindigo536; Site_l: HindIII"
201 c 203 g 90 t
                                                                                                                                                                              Score 65.2; DB 29; Length
Pred. No. 3.9e-06;
0; Mismatches 103; Indels
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/organism="Bradyrhizobium japonicum"
/wol.type="genomic DNA"
/strain="USDA110"
                                           /organism="Mycobacterium leprae"
/mol_type="genomic DNA"
/db_xref="taxon:1769"
/clone="cosmid L-373; contig 64"
/clone_lib="cordered cosmid library"
83 c 93 g 51 t
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Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University
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21376150
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Class: BAC ends
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Best Local Similarity 55.2%;
Matches 127; Conservative
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AL Submission

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDCP).

The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP prosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's pland BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

Location/Qualifiers
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BACR19D16 of RPCI-98 library from Drosophila melanogaster (fruit
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/organtsm-"Drosophila melanogaster"
/mol_type="qenomic DNA"
/db_xref="taxon:7227"
Score 55.6; DB 28;
Pred. No. 0.00099;
0; Mismatches 94;
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/note="end : TET3"
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Myler, P.J., Vogt, C., Cawthra, J., Klacking, M., Marty, A., Mack, J.,

Munden, H., Nguyen, D., Robertson, L., Sisk, E., Fazelinia, G., Aggarwal

G., Nelson, S., Seyler, A., Worthey, E. and Stuart, K.

Leishmania major Friedlin Cosmid End Sequences

Unpublished

Other-GSSs: P864c_LEISHPAC-right.1

Contact: Myler PJ

Seattle Biomedical Research Institute

4 Nickerson Street, Seatttle, WA 98109-1651, USA

Tel: 206 284-8846

Fax: 206 284-0313
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  240 GATCACCGCGCGCGCGCGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAA 299
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P864c.d_LEISHPAC-left.1 Leishmania major Friedlin Cosmid Genomic
Library Leishmania major genomic clone P864c, genomic survey
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                                                                                                                      340 BCCMCSSSSSCCGSASARGVKVRASGGAGKRGGGSGGASASHSSSSACBSSSSSCSASCW
                                                                                                                                                                                                              120 TATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCCAACGGCGCACG
                                                                                                                                                                                 180 AGTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGT
                                             900 SNSSBCSSCSSSBSSSSTSSMSSSSBSSSSGSSSSSSGTSSACVKCNASSSCGCCGCGMA
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Leishmania major
Eukaryotu; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/organism="Leishmania major"
/mol_type="genomic DNA"
/strain="Friedlin"
/db_xref="taxon:5664"
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/lab_host="E. coli ED8767"
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Seq primer: LEISHPAC-left
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BH020987
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- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifily.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Libogenic strain y2: cn bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19016 of RPCI-98 library from Drosophila melanogaster (fruit ALO53013 GI:4934461
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                                                                                                                                                                                                                                                                                                                 292 GCGCTTAACGGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGC 351
                                          CCGTTCATATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACG
                                                                       GCGCACGAGTCCAACGCG-TGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCCATCTCCACC
                                                                                                                                                                                                                            232 GGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGAC
                                                                                                                                                                                                                                                      Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                           352 GGCACGCGTACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                          853 TNGMBGTSSACSSSSCSSSVSSSKSSASSSSVSSSGSSGVS 897
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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1 Similarity 12.8%; Pred. No. 0.031;
43; Conservative 157; Mismatches 136;
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/clone_lib="RPCI-98"
/note="end : TET3"
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600AGB3TV ZM_0 7_1.5_KB Zea mays genomic clone ZMMBMa0365N21, genomic surve% sequence. CC334434.1 GB 30803847
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                                                        257 GCGCTCCGATGACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCGGTG 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STOGTCGTCGTCCTCGGAGTCGGGCGCGGAAAACGCCTCCTGCTGCT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Foaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 831)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunbergha, Robbins, D. and Lakey, N.
                                                                                                                               148 GGCCGCCGAGCGCCTGCTACGACGCGACACGCGCACACCGGAACCGGA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCA
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                                    GGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTCGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9712 Medical Center Drive, Rockville, MD 20850, Tel: 301-838-5843
Fax: 301-838-0208
Fax: 301-838-0208
Famil: whitelaw@ttjgr.org
Seq primer: TF
Class: sheared ends.
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50.1%; Pred. No. 0.086;
10e 0; Mismatches 77;
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1. 831
1. 631
1. 632
/ Organism="Zea mays"
/ mol_type="genomic DNA"
/ strain="B73"
/ db_xrae="taxon:4577"
/ clone="zwwwa035821"
/ clone="zwwwa035821"
                                                                                                                                                                                      FGACCTG 335
                                                                                                                                                                                                           Unpublished
Contact: Cathy Whitelaw
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methylation
a 280 c
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109; Conservati
                                                                                                                                                                                  317 ACGICATCICG
                                                                       208 cccccccccc
 268 ACGACGTCGTCC
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                                      GGAGCGCTCCC
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: PolyTMix
                                                                                         159 CAACAACGGCAACGGCGCACGAGGTCCAACGGGTCGGGAGCGCTCCGGCGGCAAGTCT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 634)
Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 634
/organism="Sorghum bicolor"
/mol_type="mnkn"
/db_xref="mnkn"
/db_xref="taxon:4558"
/clone_lib="bark Grown 1 (DG1)"
/clone_lib="bark Grown 1 (DG1)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda_azap; Site_l: XhoI; Site_2: EcoR!, The library was
made from poly-A RNA in the cloning vector lambda zAP II.
Clones to be sequenced were prepared by mass excision."

a 198 c 212 g 102 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukāryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoldeae; Andropogoneae; Sorghum.
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                                                                                                              13 CGAGAȚCGCCATCGCCGGCGGCCTGGTAGTCGAGGGCGCGCTCGGGGTCCGCGGCTCGCGGT 72
                                                                                                                                                                219 CGGCATCTCCACCGGCGACGTGATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCC 276
                                                                                                                                                                                      388 ACGACGTGCCGTCCCAGTAGTGGCAGCGCTTGTGCCCCCGAGCGCCCTGGCCCGTGGCGA
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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
Thent Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
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Pred. No. 0.053;
0; Mismatches 169; Indels 0
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An EST database from Sorghum: dark-grown seedlings
                   Length
                                                      Indels
                 Score 49.2; DB 28;
Pred. No. 0.037;
); Mismatches 43;
                                                      0; Mismatches
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High quality sequence start: 67
High quality sequence stop: 634
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Sorghum bicolor
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12.3%;
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Matches 150; Conservative
               Query Match
12.4%;
Best Local Similarity 63.6%;
Matches 75; Conservative
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Lubrited (02-JUN-1999) Genoscope - Centre National de Sequencage : Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Determination of this BAC-ed sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI dicestion of Drosophila DNA provided by the BDGP from the isogenic strain v2. nbw sp. the same strain used for the BDGP's pland EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSS 26-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 CAACGUGTGGTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATC 243
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 GGGAA.CGTGACATTGGCCGAGGGACCCCCGGCC 396
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/clone_lib="RPCI-98"
/note="end : T7"
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    Direct Submission
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Best Local Similarity
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Submitted (24-JUL-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and allcat@sanger.ac.uk
see http://www.ebi.ac.uk/parasites/leish.html
betails of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/
The primer sequence can be obtained from allcat@sanger.ac.uk.
Location/Qualifiers
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Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 CGAGAGCGGCATCGCCGGCGGCCTGTTAGTCGAGGGCGCGTCCGGGGTCCCGGGGTCGCGT
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Leishmania major Friedlin PAC P864 left end-sequence, genomic
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 289)
Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and
Barrell,B.G.
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                                                                                                                                                                                                                                                                      Euglenozoa; Kinetoplastida; Trypanosomatidae;
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0.084;
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/mol_type="genomic DNA"
/strain="Friedlin"
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/clone="PAC P864"
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Matches 74; Conservative
CCCCGCGCCGC 592
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Leishmania m
Eukaryota; E
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Full-length cDNA libraries and normalization
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(EDGP) -
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3-PRIME, MRNA sequence.
                                                                                                                 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNW was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          943
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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                 Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

1 (bases 1 to 1009)
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Best Local Similarity 30.8%; Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                            1. .1009
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN03P19"
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377 c 178
Drosophila melanogaster
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Contact: Genoscope
Genoscope
Genoscope- Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns of the Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6304.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BA005ZH04FPl&cluster=6304.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
Feng Liang Email: fliang@lifetech.com URL :
Feng Liang Email: fliang@lifetech.com URL :
Cgi-bin/cluster.cgi?seq=cence ID : CL0BA005ZH04FPl.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLUBA0052H04"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Yector: pCMVSPORT_6" ist strand cDNA was primed
/note="Yector: pCMVSPORT_6" ist strand cDNA was primed
with a NotI-oliq(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECORV sites of the pCMVSPORT 6 vector.
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Gryza sativa (indica cultivar-group)

Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Enhartoliodaes; Oryzeae; Oryza.

1 (bases 1 to 472)

Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E. Kudra,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

Large scale identification of ESTs involved in the interaction

between rice and Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 ATCAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCCGGTGACGTCATC 324
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22 c 56 g 173 t
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Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
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Best Local Similarity
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DB 13;
   more information about this cluster, see
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Contact: Cathy Whitelaw
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Class: sheared ends
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BX424977 Homo sapiens PLACENTA Homo sapiens cDNA clone CL0BA0052H04
3-PRIME, mRNA sequence.
BX424977.1 GI:30784421
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Li W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BPail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6304.f For
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Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
                                                                                                                                                                                                    /organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACTCGGCCACCGCGATGGCGGACGCGCTTAACGGGCATCATCCCGGT 315
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Pred. No. 0.25;
0; Mismatches 152; Indels 0
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33 c 156 g 74 t
                                                                                              FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 04 row: P column: 23
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                        89/41-9000, 02.
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                      /db_xref="taxon:39946"
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/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                          /clone_lib-"OSIIEa"
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Best Local Similarity 47.4%;
Matches 137; Conservative
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183 c
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http://www.genoscope.org.fr/

Cgi-bin/cluster.cgi?seq=CLOBA0052H04Fplscluster=6304.f. Contact:

Cgi-bin/cluster.cgi?seq=CLOBA005ZH04Fplscluster=6304.f. Contact:

Feng Liang Email: fliang@lifetech.com URL:

http://tullength.invitrogen.com/ invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID: CLOBA005ZH04Fpl.

Location/Qualifiers

irce / Organism="Homo sapiens"

/mol_type="mhRA" / Abbarday Abbarday / Clone="CLOBA005ZH04" / Abbard="Laxon:966" / Clone="CLOBA005ZH04" / Abbard="Laxon:966" / Clone="CLOBA005ZH04" / Clone="CLOBA005ZH04" / Clone="Vector: pCMYSPORT_6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoNY sites of the pCMYSPORT 6 vector.

Library was not normalized."
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., I, F., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., (,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
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methylation filtered genomic DNA library"
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Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Consortium for Maize Genomics
Unpublished
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Fax: 301-838-0208
Seq primer: TF
Class: sheared ends.
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Pred. No. 0.31;
0; Mismatches 71;
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-WODEL-frame+_p2n.model -DEF-xlp
-WODEL-frame+_p2n.model -DEF-xlp
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-NO_MAAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
                                                                             9; Search time 2356.88 Seconds (without alignments) 2291.192 Million cell updates/sec
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1 TAASDNFQLSQGGGGFAIPI......QTKSGGTRTGNVTLAEGPPA 132
           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                        nucleic search, using frame_plus_p2n model
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                                                                              September 5, 2003, 07:52:39
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Seguence:
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Insggsgryhlgptarlgcyvymgrksggtrtgnvtlaggppa"
373 c 186 t
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preventing tuberculosis
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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/mol_type="genomic DNA"
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Polypeptide nucleic sequences exported from redypeptide nucleic sequences exported from redypeptide nucleic sequences for diagnosing and Patent: WO 9909186-A 909 25-FEB-1999;
PORTNOI DENIS (FR); GUIGUENO AGNES (FR)
Location/Qualifiers
  1030 ACAGGGAACGTGACATTGGCCGAGGGACCCCGGCC 1065
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Mismatches:
Indels:
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Matches:
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Sequence 909 from Patent WO9909186.
AX005790
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//transl_table=11
/protein_id="colo5178.1"
/db_xref="GI:928796"
/db_xref="GI:9
                                                                                                                                                                                                                                                           Portnol, D. and Guigueno, A.
Polypeptide nucleic sequences exported from mycobacteria, vectors comprising same and uses for diagnosing and preventing tuberculosis Patent: WO 9909186-A 907 25 FEB-1999;
PORTNOI DENIS (FR); GUIGUENO AGNES (FR)
Location/Qualifiers
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Mycobacterium tuberculosis
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
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/organism="Mycobacterium tuberculosis"
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Matches:
                  AX005788 1068 bp
Sequence 907 from Patent WO9909186.
AX005788
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Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.

CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg. qtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon.

If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CBIO 15A Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 20, 1998 this sequence version replaced 91:2181960.
                                                                                                              Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S. V., Eiglmeler, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M. A., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Barrell, E.G.
Mycobacterium tuberculosis H37Rv
Mycobacterium tuberculosis H37Rv
Bacteria. Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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/note="Rv0119, (MTV031.13-MTCI418B.01), len: 525.fadD7,
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                                                                                                                                                                                                                                                                                     Deciphering the biology of Mycobacterium tuberculosis from the
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/mol_type="genomic DNA"
/Astrain="H37Rv"
/db_xref="taxon:83332"
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/organism="Mycobacterium
/mol_type="genomic DNA"
/strain="H37Rv"
                                                                                                                                                                                                                                                                                                         complete genome sequence
Nature 393 (6685), 537-544 (1998)
98295987
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97. .1674
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Parkhill, J.
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296071 AL121456
296071.1 GI:3242254
   1045 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCTT 1104
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Skeiky,Y., Alderson,M. and Campos-Neto,A.
Fusion proteins of mycobacterium tuberculosis antigens and their
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Sequence 1 from patent US 6544522.
AR303127
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1. .2287
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/translation-"mtkkprnpadyvigddvevsdydlkgeevyvdgerltdervegm
ASESLRLAREREANLIPGGKSLSGGSAHSPAVQVVVSKATHAKLKELARSRKMSVSKL
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HTRGVQRVRVTRNARKHRVSKHRIVAAMRHCGVPVIQEDGSLYYQGRDTSGRLTEVVA
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
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                                                                                                        complement(4399. .4401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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675.00
100.00%
100.00%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /_note=_kv012c, (MTC1418B.02c), fusA2, len: 714.
Floogation factor g, similar to eg. EFG_ECOLI P02996
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fasta scores; opt:1049 z score: 1105.5 E(): 0, 32.5%
identity in 717 aa overlap. Contains PS00017
ATP/GTP-binding site motif A (P-loop).Also similar to M.
tuberculosis fusA, MTCY210.01 (39.1% identity in 299 aa
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G (EF-G). (701 aa); 31.7% identity in 710 aa overlap."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPEGLRPDDANIMFTGGTTGLPKMVPWTHANIASSVRAIITGYRLSPRDATVAVMPLY
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YRQAWRGYHHAXPYVDIRYTLLOGRAHSVDSSDFARQMAGALALREAAAATKVILLE
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PossibleCoenzyme A-ligase similar to 4-coumarate:CoA ligase of manyorganisms e.g. pru39405_1 (537 aa). Contair PS00455butative AMP-binding domain signature. FASTA scores: gp[J39405]pru39405_1 pinus taeda xylem 4-coumarate:CoA (537 aa) opt:483z-score: 526.1 E(): 8.3e-22; 28.2% identity in 440 aaoverlap score is 0.896"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Rv0121c, (MTCI418B.03c), unknown, len: 144 aa'
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	.	gene CDS			SOD						dene	SCDS							gene	CDS				
### ##################################	81 IleThralaValAspGlyAlaBroIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100 	101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrarg 120 	121 ThrGlyAsnValThrLeualaGluGlyProProAla 132 	z	AE006925 AE000516 AE006925.1 GI:13879610	Mycobacterium tuberculosis CDC1551  ISM Mycobacterium tuberculosis CDC1551  Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales, Corvuebacterineae, Wycobacteriances, Mycobacterium, Wycobacterium		recerson, J., Deboy, K., Dodson, K., Gwinn, M., Halt, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W	Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains	Unpublished Care 1 to 14029)	Feterschinding N.D., Alland, P., Elsen, J. R., Calpenter, L., Peterson, J., DeBoy, R., Dodson, R., Gwinn, M., Haft, D., His Kolonay, J.E., Nelson, W.C., Umayam, L.A., Ermolaeva.M	Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.	ı,	rce	/organism="Mycobacterium tuberculosis CDC1551" /mol_type="genonic DNA" /crrain="Profifi"	/db_rref=_colors /db_rref=_tolors /note="c.inical strain"	gene complement(99533) /qene="MT0129"		<pre>/note="identified by Glimmer2; putative" /codon_start=1</pre>	<pre>/transl_table=11 /product="hypothetical protein" /protein_id="AAK44353.1"</pre>	/db_xref="G1:13879611" /translation="MGETDFXLRFAGSPVARLATSTPDGTPHLVPVVFALGARRPAEA TGADVIYTAVDAKRKTTQRLRRLANLEHNPRASVLVDSYADDMTQLWWVRADGYAAIH	RDGEVMRAAYRLLRAKYTQYQSVPLNGPVIAIAVQRWASRHA" gene complement(6431062) //conp="wr0130"		<pre>/note="identified by Glimmer2; putative" /codon_start=1 /transl_table=11</pre>
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603. 7970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /hote="similar to SP:P31953 GB:X57229 PID:48828
PID:1567734 PID:1877254; identified by sequence
similarity; putative"
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/db_xref="GI:13879620"
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/protein_id-"AAK44359.1"
/db_xref-"GI:13879617"
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/gene="MT0137"
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/6603. .707.
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10218. .10673
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Direct Submission
Submitted (24-MAR-2003) Garnier T., Unite de Genetique Moleculaire
Bacterienne Institut Pasteur 28, rue du Dr Roux 75724 PARIS cedex
15, France. e-Malitgarnierepasteur.fr Submitted on behalf of the
Mycobacterium bovis sequencing teams, TB Research Group, Veterinary
Laboratories Agency WeyDridge, Woodham Lane, New Haw, Addlestone,
Surrey KT15 3NB, UK. Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 15A, UK. PT4 Annotation, Genopole, Institut
Pasteur, 28 Rue du Docteur Roux, 75724 Paris Cedex 15, France.
Unite du Docteur Roux, 75724 Paris Cedex 15, France.
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Pryor,M., Duthoy,S., Grondin,S., Lacroix,C., Monsempe,C., Simon,S.,
Harris,B., Atkin,R., Doggett,J., Mayes,R., Keating,L.,
Wheeler,P.R., Barkhill,J., Barrell,B.G., Cole,S.T., Gordon,S.V. and
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Mycobacterium bovis subsp. bovis AF2122/97
Mycobacterium bovis subsp. bovis AF2122/97
Bacteria, Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterinae; Mycobacteriaceae; Mycobacterium; Mycobacterium
tuberculosis complex.
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BX248334.1 G1:31616762
Complete genome.
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//Jocus_tag="Mub0001, dnaA, len: 507 aa. Equivalent to Rv0001, len: 507 aa, from Mycobacterium tuberculosis strain H37Rv, 199.6% identity in 507 aa overlap). dnaA, chromosomal replication initiator protein (see citations below), equivalent to other Mycobacterial CHROMOSOMAL REPLICATION INTIATOR PROTEINS e.g. P64388 DNAA_MYCLE from Mycobacterium leprae (502 aa); 09L7L7|DNAA_MYCRA from Mycobacterium paratuberculosis (509 aa); P49992|DNAA_MYCRA from Mycobacterium sneamatis (504 aa); etc. Also highly similar to others except in N-terminus e.g. 092H75|DNAA_SYRCH CHROMOSOMAL REPLICATION INTIATOR PROTEIN from Streptomyces ofbrysomallus (624 aa); 092H76|DNAA_STRRE from Streptomyces ofbrysomallus (624 aa); DNAA_ECOLI|P03004|B3702 chromosomal replication initiator protein from Escherichia coli strain K12 (467 aa); PASTA scores: opt: 986, E(): 0, (43.2% identity in 389 aa overlap); etc. Contains PS00017 ATP/CTP-binding site motif A (P-loop) and PS01008 DnaA protein signature. BELONGS TO THE DNAA FAMILY. Note that the first base of this gene has been taken as base 1 of /codon_start=1 lable-11
//codon_start=1 lable-11
//codon_start=1 lable-11
//codon_start=1 lable-11
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2052. 3260
/gene="dnaN"
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//ocus_taq="Mb0003"
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                                                                                                                                                                                                                                                                    LPMLTGIRVEILGETVVLAATDRFRLAVRELKWSASSPDIEAAVLVPÄKTLAERAKÄG
GGSDVRLSEGGGPGVGKDGLLGISGKKRSTFLLDAEFRRRQLLEPHTAVATMD
VAELIEA KLIVALVADRGAOVRMEFADGSVRLSAGADDVGRAEDDLVVDYAGEPLTIA
RNPTYLTDGLSSLRSERVSFGFTTAGKPALLRPVSGDDRPVAGLNGNGPFPAVSTDYV
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YSTTLGSHRVSADLPLIRVGTDRAVISTIVVNDGRECAVDLEIATGRVNKARLNRSSV
RSTRDVVGVLRAVLFAPEDLGLVRGDPADRRRYLDDLAIVRRPAIAAVRAEYERVVRQ
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RDDLILRLGDQPAKGFASHGEAWSLAVALRLAAYQLLRVDGGEPVLLLDDVFAELDVM
RRRALATAAESAEQVLVTAAVLEDIPAGWDARRVHIDVRADDTGSMSVVLP"
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RGRVASVASGRVAGRRRSWSGPGPDIRDPQPLGKAARELAKKRGWSVRVAEGMVLGQW
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/NDCLEOTIDYLTRANSFERSES"
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(SINGLE-STRAND DNA BINDING PROTEIN)*
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                                                                           /gene= yt.p //gene="Mb0005" //gene="5.99.1.3" //gene="Mb0005, gyrB, len: 714 aa. Equivalent to Rv0005, len: 714 aa. from Mycobacterium tuberculosis strain H37Rv, 190.9% identity in 714 aa overlap). gyrB, DNA gyrase subunit B (EC 5.99.1.3) (see citations below), equivalent, except in N-terminus, to other Mycobacterium laprae (697 aa); 091713|GYRB_MYCPA from Mycobacterium avium subsp. paratuberculosis (677 aa) (has its N-terminus shorter); P48355|GYRB_MYCSA from Mycobacterium smegmatis (675 aa); etc. Also highly similar to others e.g. 710069 from Streptomyces coelicolor (686 aa); P50075|GYRS_STRSH from
                                                                                                                                                                                                                                                                                                                                                                   152248 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 152307
SAVVGHQIAEHARPTALNDGVLSVIAESTAWATQLRIMQAQLLAKIAAAVGNDVVRSL
KITGPAAPSWRKGPRHIAGRGPRDTYG"
5123. .7267
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Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of
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Sequence 4 from patent US 6290969.
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AR169152.1 GI:17906927
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                                          /locus_tag="Mb0005"
5123. .7267
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(Dasse; 1 to 447)

Reed, S.G., Skefky,Y.A.W., Dillon,D.C., Campos-Neto,A., Houghton,R., Vedvick,T.S. and Twardzik,D.R.
Compounds and methods for diagnosis of tuberculosis
Patent: US 6338852-A 4 15-JAN-2002;
Location/Qualifiers
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Sequence 4 from patent US 6338852.
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AR182442.1 GI;20225649
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       Location/Qualifiers
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Patent: US 62,90969-A
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1 (bases 1 to 447)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C. Compounds and methods for diagnosis of tuberculosis
Patent: US 6458366-A 4 01-OCT-2002;
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Reed, S.G., Skelky, Y.A.W. and Dillon, D.C.
Compositions and methods for the prevention and treatment of
tuberculosis infection
Patent: US 6350456-A 4 26-FEB-2002;
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                                                                                       Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R. and Lodes, M.J. Compounds and methods for diagnosis of Tuberculosis Patent: JP 2001500383-A 4 16-JAN-2001; CORIXA CORP
                                                                                                                                                                               OS Unidentified
PN JP 2001500383-A/4
PD 16-JAN-2001
PF 07-071997 JP 1998518432
PR 11-OCT-1996 US 08/725622,13-MAR-1997 US
STEVEN G REED!YASIR A W SKEIKY,DAVIN C DILLON, PI
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Location/Qualifiers

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Corganism="unidentified"

/organism="unidentified"
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/do.scef="taxon:32644"

July corganism="unidentified"
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16-AN-2001
07-OCT-1997 UP 1998518432
11-OCT-1996 US 08/729622
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Compounds and methods for immunotherapy and diagnosis of
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Patent: EP 1203817-A 4 08-MAY-2002;
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
1 146 c 149 g 7;
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Sequence 4 from Patent EP1203817.
AX429596
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BD069285 447 bp DNA linear PAT 27-AUG-2002 Compounds and methods for immunotherapy and diagnosis of
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12-JUL-1996 US 08/680574
PI STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS
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              11 ACGCCCCCTCCGATAACTTCCAGCTCTCCCAGGGTGGCAGGGATTCGCCATTCCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                   08/533634
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PC C12N1/21//A61K39/04, (C12N1/21, C12R1:19)
CC Strandedness: Single;
CC Topology: Linear;
CC Topology: Linear;
CC Compounds and methods for immunotherapy and diagnosis or
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08/620874,05-JUN-1996 US 08/659683 PR
08/680574
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Reed,S.G., Skeiky,Y.A.W., Dillon,D.C., Neto,A.C., Houghtc Vedvick,T.H. and Twardzik,D.R.
Compounds and methods for immunotherapy and diagnosis of Patent: JP 2001517069-A 4 02-OCT-2001;
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JP 2001517069-A/4
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30-AUG-1996 JP 1997511464
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BD069285.1 GI:22614888
JP 2001517069-A/4.
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DUND0445 COMPOUNDS and methods for immunotherapy and diagnosis of Tuberculosis.
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MICHAEL J LODES
PC C12N15/31, C07K14/35, A61K39/04, A61K48/00, A61K49/00, C12N15/62, PC C12N15/31, C07K19/00, C12N1721, E
                                                                                                                                               Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R. and Lodes, M.J.
Compounds and methods for immunotherapy and diagnosis of Patent: JP 2001501832-A 4 13-FEB-2001;
CORIXA CORP
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PN JP 2001501832-A/4
PD 13-FEB-2001
PP 07-0CT-1997 JP 1998518456
PR 11-OCT-1996 US 08/730510,13-MAR-1997 US
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, PI
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Strandedness: Single;
Topology: Linear;
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JP 2001501832-A/4.
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Qy 61 Db 191	61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80 	Oy 12
Oy 81 Db 251	81 IleThralaValaspGlyAlaProIleasnSerAlaThralaMetAlaAspAlaLeuasn 100 	Search compl Job time : 2
Qy 101 Db 311	1 GlyhishisProGlyAspVallieSerValThrTrpGlnThrLySSerGlyGlyThrArg 120 	
Oy 121 Db 371	1 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132 	
RESULT 15 AR169165 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AR169165 167-2001 Sequence 17 from patent US 6290969. AR169165.1 GI:17906947 UNRNOWN.	·
REFERENCE AUTHORS TITLE	Unclassified.  1 (bases I to 1872)  Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S. and Twardzik, D.R. Compounds and methods for immunotherapy and diagnosis of	
JOURNAL FEATURES SOUICE BASE COUNT ORIGIN	Patent: US 6290969-A 17 18-SEP-2001; Location/Qualifiers 11872 /organism="unknown" 318 a 616 c 604 g 332 t 2 others	
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: DB:	ores: 1.35e-41 Length: 1872 670.00 Matches: 131 larity: 99.24% Conservative: 0 imilarity: 99.26% Mismatches: 1 6 Gaps: 0	
US-09-684-21	US-09-684-215A-4 (1-132) x AR169165 (1-1872)	•
0y 1 Db 758	1 ThralaalaseraspasnPheGlnLeuserGlnGlyGlyGlnGlyPheAlaileProile 20	·
Qy 21 Db 818	21 GlyginalametalailealaglyginileargserglyglyglyserProThrvalHis 40 	
Qy 41 Db 878	41 IleGlyProThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60 	
Oy 61 Db 938	61 ValGinargValValGijSeralaProalaAlaSerLeuGijyileSerThrGijAspVal 80 	
Qy 81 Db 998	81 IleThralavalaspGlyAlaProIleasnSerAlaThralaMetAlaAspAlaLeuAsn 100 	
Qy 101 Db 1058	1 GlyhishisproglyaspvallieServalthrfrpglnThrLysSerGlyGlyThrarg 120 	`
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Title: Perfect :

Sequence:

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Run on:

Scoring table:

Total number

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Sequence 1, Application US/09223040

Patent No. 6544522

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasir

APPLICANT: Alderson, Mark

APPLICANT: Campos-Neto, Antonio

APPLICANT: Corixa Corporation

ITILE OF INVENTION: Fusion Proteins of Mycobacterium tuberculosis Antigens

TILE OF INVENTION: and Their Uses

FILE REFERENCE: 014058-009010US

CURRENT APPLICATION NUMBER: US/09/223,040

CURRENT FILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                        Sequence 332, Sequence 332, Sequence 188, Sequence 352, Sequence 352, Sequence 336, Sequence 336, Sequence 316, Sequence 312, Sequence 316, Se
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OTHER INFORMATION: protein Ral2-TbH9-Ra35
NAME/KEY: modified_base
US-09-643-597-353

US-09-6643-597-351

US-09-643-597-351

US-09-643-597-351

US-09-606-412B-351

US-09-508-419-348

US-09-598-419-348

US-09-598-419-348

US-09-598-419-332

US-09-598-419-332

US-09-598-419-332

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US-09-598-419-336

US-09-598-419-336

US-09-598-419-316

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        Command line parameters:
-WODEL-frame+_p2n.model -DEV-x1p
-Q-/cgn2_1/USPTO_spool_p/US09684215/runat_05092003_072203_593/app_query.fasta_1.853
-Q-/cgn2_1/USPTO_spool_p/US09684215/runat_05092003_072203_593/app_query.fasta_1.853
-Q-/cgn2_1/USPTO_spool_p/US09684215/runat_05092003_07203_593/app_query.fasta_1.853
-LOOPEXT-0 -UNITS-blts -START-1 -END--1 -WATRIX=blosum62 -TRANS=human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE=-pct -THR_MAX-100 -THR_MIN-0 -ALIGN=-150
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-NO_MARP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DSV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPDP=10 -XGAPEXT-0.5 -FGAPOP=6
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-09-056-556-4

US-09-056-556-4

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US-08-818-112-17

US-08-818-112-17

US-08-818-112-17

US-09-056-556-17

US-09-056-556-17

US-09-073-556-17

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Copyright (c) 1993
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Sequence 2, Application US/09103840A

Patent No. 6294328

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: WINTE, Owen R.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

UNMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2.
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ORGANISM: Mycobacterium tuberculosis
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Patent NO. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: PRASER, Clair e M.
APPLICANT: WHITE, Owen R.
APPLICANT: WINTER, John C.
TITLE OF INVENTION: DNA, SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: 1998-06-24
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2.
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                                                  152164 GTCCAACGCGTGGTCGGGAGCGCTCCGGCGGCGAAGTCTCCGCCATCCCACCGGCGACGTG
                                                                                                                                                                                                                                                                                          ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                            101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg
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                                                                                                                                                                  61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
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Mismatches:
Indels:
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Query Match:
DB:
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US-09-103-840A-1
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191 Grccaacgcgrcggagcgcrccggcgcaagrcrcggcarcrccaccggcgacgrg 250
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                                                                        21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
1 ThralaalaseraspasnPheGlnLeuSerGlnGlyGlnGlyPhealalleProIle
                                    11 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGTGGGCAGGGATTCGCCATTCCGATC
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APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08818111; Patent No. 6338852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-631
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 447 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
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CITY: Seattle
STATE: Washingt
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US-08-818-111-4
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                                    152115 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCGCACGCGT 152174
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                ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80
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OF TUBERCULOSIS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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6300 Columbia Center, 701 Fifth Avenue
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31.392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID.NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDENNES: single
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Matches:
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APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METITLE OF INVENTION: AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                       US-08-818-112-4
Sequence 4, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
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ADDRESSEE: SEED and E
STREET: 6300 Columbia
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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Best Local Similarity:
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US-08-818-112-4
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131
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MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC Compatible
OPERATING SYSTEM: EC-DOS/MS-DOS
SOFTWARE: PatentinfRelease #1.0, Version #1.30
CURRENT APPLICATION DĀTA:
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Conservative:
Mismatches:
Indels:
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CITY: Seattle
STATE: Washington
ZTOUTRY: USA
                                                                                               Length:
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APPLICANT: Skeiky, Wasir A.W.
APPLICANT: Dillon, Dgvin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Thomiel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendricksön, Ronald C.
TITLE OF INVENTION: GOMPOUNDS AND MENUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
                                                                                           7. 8e-62
670.00
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99.24%
 LENGTH: 447 base pairs
TYPE: nucleic acid
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              ; TYPE: nucleic aci
; STRANDEDNESS: sir
; TOPOLOGY: linear
US-09-056-556-4
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                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                11 ACGCCCCCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCCCCATTCCCGATC 70
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                                                                                                                                   1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/0905656
Patent NO. 6350456
GENERAL INFORMATION:
APPLICANT: Read, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: WEAL

ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RC-Base #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,556

FILING DATE: 07-APR-1998

CLASSIFICATION:
              447
131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
            Length:
Matches:
Conservative:
Mismatches:
                                                                                                         US-09-684-215A-4 (1-132) x US-08-818-111-4 (1-447)
                                                                 Indels:
                                                                                Gaps:
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NAME: MAK!, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
                      670.00
99.24%
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99.26%
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STATE: Washington
                                       Percent Similarity:
Best Local Similarity:
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STREET: 63
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-056-556-4
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                                                                                                                          OPERATING SYSTEM: COMPACTORS OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE: US/08/818,112
FILING DATE: 13-MAR-1997
   Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-684-215A-4 (1-132) x US-08-818-112-17 (1-1872)
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-818-111-17; Sequence 17, Application US/088181111; Patent No. 6338852; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.79e-61
670.00
99.24%
99.24%
   6300 Columbia
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                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                     Seattle
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-08-818-112-17
                                                                  98104-7092
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Best Local Similarity:
                                                                                                                                                                                                            CLASSIFICATION:
                                                    USA
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                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 ACGCCCCCTCCCGATAACTTCCAGCTGTCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHODS FOR IMMUNOTHERAPY OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                      447
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Matches:
Conservative:
Mismatches:
Indels:
APPLICALL...
FILING DATE: 05-MAY-LDD.
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MARI, David J.
REGISTRATION NUMBER: 210121.417C9
FELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
LENGTH: 447 base pairs
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-684-215A-4 (1-132) x US-09-072-596-4 (1-447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Resiry, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND MET
TITLE OF INVENTION: COMPOUNDS AND MET
TITLE OF INVENTION: COMPOUNDS OF NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERDY ITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/08818112 Patent No. 6290969
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670.00
99.24%
99.24%
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Query Match:
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US-08-818-112-17
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81 IleThralaValaspGlyAlaProIleAsnSeralaThralaMetalaAspAlaLeuAsn 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            878 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACACACAACGGCAACGGCGCACGA
                                                                                                                                                                                     COMPOUNDS AND METHODS FOR THE PREVENTION AND
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUW TYPE: FIDPPY disk
COMPUTER: IBM PC COMPatible
COMPUTER: IBM PC COMPatible
COMPUTER: STRIM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: O7-APR-1998
CLASSIFICATION:
ATYORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
INFORMATION POR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1072 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
                    1118 ACAGGGAACGTGACATTGGCCGAGGGACCCCGGCC 1153
                                                                                                                                     APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Steiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
    121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
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Matches:
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                                                                             US-09-056-556-17
; Sequence 17, Application US/09056556
; Patent No. 6350456
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99.24%
99.24%
99.24%
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                                                                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washingtor
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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CITY: Se
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                                                                                              TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos retto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                              OF.
                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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99.24%
99.24%
99.26%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                   Washington
                                                                                                                                                    STREET: 6300 CO. CITY: Seattle STATE: Washingto COUNTRY: USA
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Best Local Similarity:
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81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                                                                                                                                                    61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Carter, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Ran, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1862, Application US/09736457 Patent No. 6509448
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Bangur, Chaitanya S.
Lodes, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       632.00
96.21%
95.45%
93.63%
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US-09-736-457-1862
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-736-457-1862
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                                               998 ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACGCGATGGCGGACGCGCTTAAC 1057
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                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reed, Steven G.
APPLICANT: Reel, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                               1118 ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                    121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
Conservative:
Mismatches:
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MARI, DAVId J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21012
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEPAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/09072596
Patent No. 6458366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.79e-61
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CITY: Seattle
STATE: Washington
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ZIP: 98104-7092
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Oy 101 GlyHisHisProGlyAspValileSerValThrTrpGlnThrLysSerGlyGlyThrArg 120	370 ACAGGAACGTGACATTGGCCGAGGGACCCCGGCC	US-09-606-421B-353; Application US/09606421B; Sequence 353, Application US/09606421B; Patent No. 6531315; GENERAL INFORMATION:	APPLICANT: Wangy Tongrong  APPLICANT: Fan, Liqun  APPLICANT: Kalos, Michael D.  APPLICANT: Bangur. Chaltanya S.  APPLICANT: Hosken, Wancy  APPLICANT: Fanger, Gary R.  APPLICANT: Li, Samuel X.  APPLICANT: Wanca Aliun	APPLICANT: Skelky, Yasir A.W.  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  FILE REFERENCE: 210121 455C9  CURRENT APPLICATION NUMBER: US/09/606,421B  CURRENT FILING DATE: 2000-06-28	; NUMBER OF SEQ ID NOS: 358 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 353 ; LENGTH: 900 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-606-421B-353	Alignment Scores: 1.78e-57 Length: 900 Pred. No.: 632.00 Matches: 126 Score: 96.21% Conservative: 1 Best Local Similarity: 95.45% Mismatches: 1 Query Match: 43.63% Indels: 4 DB:	-09-684-215A-4 (1-132) x US-09-606-421B-353 (1-900)	Oy 1 ThrAlaAlaSerAspAsnPheGinLeuSerGinGiyGijGinGiyPheAlaleProlle 20	Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40"	Oy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60	Oy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80	Oy 81 IleThralavalaspGlyalaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100	Oy 101 GlyhishisProGlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120	Oy 121 ThrGlyAsnValThrLeualaGluGlyProProAla 132 
Db 190 GTCCAACGCGTCGGGAGCCTCCGGCGAAGTCTCGGCATCTCCACCGCGACGTC 249  Qy 81 IleThralaValAspClyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100  LHIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	101 GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg	Qy 121 ThrGlyAsnValThrLeualaGluGlyProProAla 132 		APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:	; APPLICANT: Sketky, Yasir A.W. ; APPLICANT: Henderson, Robert A. ; APPLICANT: Henderson, Robert A. ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER ; FILE REFERENCE: 210121.455011 ; CURRENT APPLICATION NUMBER: US/09/643,597	NUMBER OF SEC 1D NOS: 369 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ 1D NO 353 ; LENGTH: 900 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-643-597-353	ent Scores: 1.78e-57 No.:	Score: 632.00 Matches: 126 Percent Similarity: 96.21% Conservative: 1 Best Local Similarity: 95.45% Mismatches: 1 Query Match: 4	4 32) x US-09-643-59	Qy 1 ThralaalaSerAspAsnPhedlnLeuSerGlnGlyGlyGlnGlyPhealaIIeProIle 20 	Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40	Qy 41 IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60 	Oy 61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGly1leSerThrGlyAspVal 80 	Qy 81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100

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81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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APPLICANT: Retter, Marc
APPLICANT: Rannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aij
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RESULT 15
US-09-736-457-1861
; Sequence 1861, Application US/09736457
; Patent No. 6509448
                                                                                                                                                           Wang, Tongtong
Bangur, Chaitanya S.
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
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APPLICANT: Wang, T
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Search completed: September 5, 2003, 12:11:59 Job time: 951.552 secs

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Command line parameters:
-MODEL-framet-p2n, model -DEV-x1p
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-DB-N_Geneseq_19Jun03 -OEMT-fastap -SUFFIX-rng -MINMATCH-0.1 -LOOPCL-0.
-LOOPEXT-0 -UNITS-b1ts -START-1 -END--1 -MATRIX-b10sum62 -TRANS-human40.cdi
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-USER-US09684215_eCGN_1 1_626_erunat_05092003_072201_548 -NCPU-6 -ICPU-3
-NO_MMAP -LARGQUERY NEG_SCORES-0 -WAIT -DSPEDCKC+100 -LONGLOG
-FRAPOUT-120 -WARN TIMEOUT-30 -THREADS-1 -XGAPOP=10 -XGAPEXT-0.5 -FGAPOP=6
-FGAPEXT-7 -YGAPOP=10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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| SIDS1/gcgdata/geneseq-embl/NA1980.DAT:*
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1 TAASDNFQLSQGGGGFAIPI......QTKSGGTRTGNVTLAEGPPA 132
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                            nucleic search, using frame_plus_p2n model
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Maximum DB seq length: 200000000
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Mycobacterium spec Mycobacterium tube Mycobacterium tube Mycobacterium sp. Mycobacterium spec Nucleotide sequenc M. tuberculosis an M. tuberculosis re M. tuberculosis DN M. tuberculosis an M. tuberculosis re M. tuberculosis DN Mycobacterium tube Mycobacterium spec Mycobacterium tube Human /M. tubercul Ral2-P510S-C const Nucleotide sequenc Nucleotide sequenc Mycobacterium tube Nucleotide sequenc DNA encoding antig M. tuberculosis im Mycobacterium tube Description and is derived by analysis of the total score distribution ALIGNMENTS SUMMARIES AA199683 AAL40769 AAD28343 AAD47083 AAD28342 AAD47110 AAT91466 AAZ19265 AAD28335 AAD47078 AAT91403 AAS03780 AAD47080 AAS64132 AAS03781 AAL40769 standard; DNA; 396 DB 2190 2190 2191 2286 2287 2287 2287 2287 Length Query 1000.0 1000.0 1000.0 1000.0 Score RESULT 1

Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds. Nucleotide sequence encoding Ral2 protein. 03-OCT-2002 (first entry) 

AAL40769;

Unidentified

Location/Qualifiers

Key

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

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fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to be useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The cooling sequence can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                                                                                                                                                                                                                                                                                                                                           Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyBheAlaIleProIle
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Mismatches:
                              /product= "Ral2 protein"
/note= "No start or stop codon"
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                                                                                  WO200125401-A2
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fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 kpa C-terminal fragment of serine protease antigen MTB32A of Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokamyotic origin and to encode a protein product for use as an antigen for defecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to Gusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
120
                                                                   Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide
                                                   101 GlyHisHisPfcGlyAspvalIleSerValThrTrpGlnThrLysSerGlyGlyThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a recombinant nucleic acid molecule encoding
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                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence encoding Ral2-mammaglobin fusion protein.
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/product= "Ral2-mammaglobin fusion protein"
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                                                                                                                      121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                          Location/Qualifiers
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- Unidentified.
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P-PSDB; AA022141.
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Example; Fig 13A-B; 83pp; English.
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                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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98US-0223040.
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P-PSDB; AAY32071.
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                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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30-DEC-1998;
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This DNA sequence includes a coding region for a recombinant Wycobacterium fubrculosis bi-antigen fusion protein (see AAY32071), termed Mtb24, composed of the antigens Ral2 and DPPD. The Lusion brotein (see AAY32071), DNA is useful for the recombinant production of the fusion protein. Coding sequences for the antigens were modified by PCR in order to facilitate their fusion and subsequent expression of the fusion protein. The invention provides fusion proteins or protein, and then ligated. The invention provides fusion proteins can protein at least 2 M. tuberculosis antigens. The new fusion proteins and polynucleotides encoding them are useful as vaccines for preventing tuberculosis (claimed), for diagnosis (via tuberculosis antibodies), monitoring of disease progression, and treatment of tuberculosis. They are more effective immunogens than mixtures of the individual protein components.
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Matches:
Conservative:
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Best Local Similarity:
Query Match:
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/iransl_except= (pos:694..696, aa:Xaa)
/note= "No start or stop codon. Xaa= In frame stop codon"
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/transl_except= (pos:353..355, aa:Xaa)
/transl_except= (pos:353..357, aa:Xaa)
/transl_except= (pos:367..377, aa:Xaa)
/transl_except= (pos:701..702, aa:Xaa)
/transl_except= (pos:101..702, aa:Xaa)
/note= "This codon has an apparent 1 nucl
which alters the reading frame.
                                                                                                                                                                                                                                                  DNA encoding antigenic fusion protein Ral2-DPPD (Mtb24).
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/product= "Mtb24 #3"
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98US-0056556.
98US-0223040.
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(SKEI/) SKEIKY
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01-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                             Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 IleGlyProThralaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant nucleic acid molecule encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represents the DNA encoding the Ral2-DPPD fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 702 BP; 127 A; 229 C; 225 G; 121 T; 0 other;
          4.696
/*tag= a
/product= "Ral2-DPPD fusion protein"
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 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             Example 1; Fig 3; 39pp; English.
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675.00
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                                                                                                                 06-OCT-2000; 2000WO-US27652
                                                                                                                                            99US-0158585
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P-PSDB; AA022139.
                                                                                                                                                                     (CORI-) CORIXA CORP.
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Best Local Similarity:
                                                              WO200125401-A2
                                                                                                                                            07-OCT-1999;
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                                                                                                                                      The invention relates to a purified polypeptide which induces an immune response of Mycobacterium tuberculosis. Polypeptides of the invention are useful for diagnosing, treating or preventing M. tuberculosis infection, particularly tuberculosis infection. In particular, the polypeptides are useful as a vaccine formulation with an adjuvant to afford long-term protection in animals against the development of tuberculosis. The protein coding sequence may be used to encode a protein product for use as an immunogen to induce and/or enhance an immune response to M. tuberculosis. This sequence represents DNA encoding an M. tuberculosis fusion protein of the invention. This polymucleotide encodes 3 different proteins, each in a different reading frame.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                 New fusion proteins of Mycobacterium tuberculosis antigens, useful diagnosing, treating or preventing M. tuberculosis infection, particularly as vaccine for treating or preventing tuberculosis
                                       Ä
                                       Campos-Neto
                                                                                                                                                                                                                                                       C; 225 G; 121 T; 0 other;
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Matches:
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                                                               P-PSDB; AAU74600, AAU76541, AAU76542.
                                     Dillon DC,
                                                                                                                        Examples; Fig 13; 62pp; English
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DILLON D C.
ALDERSON M.
CAMPOS-NETO A.
                                     Reed SG, Skeiky YA,
                                                       WPI; 2002-171134/22
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(DILL/)
(ALDE/)
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Mycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis mature Ra35 (N-terminus of MTB32A; RA35FL) antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis
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                                                                                                          immunity; diagnostic agent; gene therapy; Ra35 antigen;
                                                   mature Ra35 antigen encoding
                                                                                                                                                                                                                                         Location/Qualifiers
4..996
/*tag=
/*rad=
/product= "Ra35 mature antigenic prote:
/transl_except= (pos:547..549, aa:Asp)
/transl_except= (pos:550..552, aa:Ser)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guderian J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP; 169 A; 331
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                                                   Mycobacterium tuberculosis
                                                                                                                                                                                        Mycobacterium tuberculosis.
(first entry)
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                                                                                                          Vaccine;
                                                                                                                                       gene; ds
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                                                                                     777
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                                                                                                                                                                                                                                                                                                                               Vaccine; immunity; diagnostic agent; gene therapy; Ra35FLMutSA; mutant; gene; antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tuberculosis.
                                                       IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg
                       ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGACGGCGCACGA
                                           ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal
                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis Ra35FLMutSA mutant antigenic protein DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "Ra35FLMutSA mutant antigenic protein"
                                                                                                                                                                                      ACAGGGAACGTGACATTGGCCGAGGGACCCCCGGCC 993
                                                                                                                                                                           121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 80-81; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
4..996
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P-PSDB; AAE29703.
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as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis Ra35FLMutSA mutant antigenic protein encoding DNA.
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/transl_except= (pos:547..549, aa.Asp)
/transl_except= (pos:550..552, aa.Ser)
                                                             Sequence 1002 BP; 169 A; 331 C; 341 G; 161 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
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                                                                                             Scores
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                                                                                                                                                                                                                                      The present invention relates to fusion proteins containing at least
two Mycobacterium species antigens, nucleotides encoding them and
compositions comprising such fusion proteins. The present invention
particularly relates to nucleic acids encoding fusion proteins that
include two or more individual M. tuberculosis antigens which increase
include two or more individual M. tuberculosis antigens which increase
the serological sensitivity of sera from individuals infected with
tuberculosis and methods for their use in adiagnosis, prevention and
treatment of tuberculosis inferction. Sequences of the invention are
useful for eliciting an immune response in a mammal, e.g., human,
immunised with BGC. They are useful in the diagnosis, treatment and
prevention of Mycobacterium infection. The fusion proteins and the
polynucleotides are useful as diagnostic tools in patients infected
with Mycobacterium, in vitro and in vivo assays for detecting humoral
antibodies or cell-mediated immunity against M. tuberculosis, for the
continuogens to generate or elicit a protective immune response in a
patient and for rasising anti-M. tuberculosis antibodies in a non-human
continuodens of the protective immune response in a
patient and for rasising anti-M. tuberculosis antibodies in a non-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       718 ATCGGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGCACGA 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ention are useful as in vivo diagnostic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTB32A
                                                                                                                                             Composition comprising WTB39 antigen and WTB32A antigen from Mycobacterium species, useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           animal. Sequences of the invention are also used as vaccines. fusion proteins of the invention are useful as in vivo diagnos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1002 BP; 169 A; 331 C; 342 G; 160 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium species MTB32A (Ra32FL) mature protein.
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                            Disclosure; Page 95; 136pp; English.
                                                             Reed S, Alderson M;
01-FEB-2001; 2001US-265737P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.89e-56
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                                                                                             WPI; 2002-147798/19.
                                (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nucleic acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with the serological sensitivity of sera from individuals infected with treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention and useful for eliciting an immune response in a mammal, e.g., human, immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected with Mycobacterium, in vitro and in vivo assays for detecting humoral antibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogens to generate or elicit a protective immune response in a patient and for raising anti-M. tuberculosis antibodies in a non-human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; Ra32FLMutSA; mutant; mutein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; 341 G; 161 T; 0 other;
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121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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4..96
/*tag= a
/product= "Ra35FLMutSA protein"
                                      Mycobacterium species Ra35FLMutSA mutant cDNA
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IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
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                                                                                                                                                                                                                                                                                                                                             proteins from various Mycobacterium species microorganisms. The nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
    Sequences AAX34001-X34252 represent nucleic acids encoding secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted protein; Mycobacterium; primer; PCR; amplification; hybridisation; detection; vaccine; immunisation; infection; s
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Matches:
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14-AUG-1997;
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                                                                               GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg
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Indels:
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Goguet de la Salmoniere Y;
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                                                                                                 Sequences AAX34001-X34252 represent nucleic acids encoding secreted proteins from various Mycobacterium species microorganisms. The nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in vaccines for immunisation against a bacterial or viral infection.
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                                               Mycobacterial DNA vectors containing reporter constructs identifying coding or promoter sequences involved in infection-associated protein expression
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AIDS; acquired immunodeficiency disease; His Tag;
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Matches:
Conservative:
Mismatches:
Indels:
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Portnoi D,
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Pelicic V,
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P-PSDB; AAY04830.
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Best Local Similarity:
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       Guigueno A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence encodes Mycobacterium tuberculosis fusion protein, TDRA12-HTC4H and includes a His tag at the N-terminus to aid purification. Compositions comprising at least 2 heterologous antigens, as a fusion protein, and vectors expressing the fusion proteins are used as vaccines to prophylactically immunise mammals (especially humans) against infection by Mycobacteria. The compositions contain at least 2 heterologous antigens that increase the serological sensitivity of individuals infected with tuberculosis, a disease frequently affecting patients with acquired immunodeficiency disease,
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                                                                                                                             ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccinating against Mycobacteria infections in mammals using fusion proteins comprising combinations of heterologous antigens
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                                                    /product= "TDRA12-HTCC#1"
/transl_except= (pos:1621..1623,aa:Xaa)
/note= "Xaa= In frame STOP codon"
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/note= "Region derived from Thrombin"
445..1629
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Matches:
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Gaps:
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ocation/Qualifiers
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Gaps:
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89..1156
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                                                                                                        1.5e-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion polypeptide, comprising a polynucleotide sequence of Ra12, a 14 KDa C-terminal fragment of serine protease antigen MTB32A of Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both ewkaryofic and prokaryofic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that
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                                                                                                                                                                                                                                                                                                  Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
immunogen; cytokine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide
        81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn
                                                                                                                          GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg
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                                                                                                                                                                                                                                                                                  fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                         /product- "Ra12-WT1 fusion protein"
                                                                                                                                                                           ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                                                                                                                                                                                                                                                                  sequence encoding Ral2-WT1
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4..1740
/*tag= a
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the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynuclectide sequence represents the DNA encoding the Ral2-WTI fusion protein.
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                                                                                                                                                                                    Sequence 1742 BP; 372 A; 569 C; 490 G; 311 T; 0 other;
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Matches:
Conservative:
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Indels:
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US-09-684-215A-4 (1-132) x AAD47084 (1-2190)
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                1118
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                                                RESULT 15
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                                                                                           The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 kba C-terminal fragment of serine protease antigen MTB32A of a 14 Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is indected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCACCGCGGTCGACGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 1057
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                                                                                                                                                                   Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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Mismatches:
Indels:
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Matches:
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06-OCT-2000; 2000WO-US27652
                                                                                         Skeiky Y, · Guderian J;
                                                            (CORI-) CORIXA CORP
                                                                                                                      WPI; 2001-266299/27.
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                            07-OCT-1999;
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynucleotide sequence encoding an antigen or an antigenic fragment from Wycobacterium sp. and a Leishmania polynucleotide sequence encoding a polypeptide or its fragment. The Leishmania polynucleotide is selected from TSA, LeIF, MIS, and 6H polynucleotides. Sequences of the invention are used in methods for elliciting immune response in mammals. They are useful as vaccines to ellicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynucleotides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is a DNA encoding MTB72F fusion protein of from M. tuberculosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, M15 or 6E polynucleotide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and
                                                                                                                                                                                                                                                                                                                                                                                    gene therapy; TbH9; antigen;
                                                                                                                                                                                                                                                                                                                            Mycobacterium sp. MTB72FMutSA fusion protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "MTB72FMutSA fusion protein"
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                      Ra35MutSA; Ra12; MTB72MutSA; chimeric; gene; ds
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    Mycobacterium sp.
    Mycobacterium tuberculosis.

                                                                                                                                                                                                                                                                                                                                                                                       Vaccine; immunity; diagnostic agent;
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P-PSDB; AAE29709.
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ThrGlyAsnValThrLeuAlaGluGlyProProAla 132 	121 ThrGlyAs         382 ACAGGGAA
	111111 322 GGGCATCA
GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120	101 GlyHisHi
ATCACCGCGGTCGACGCGCTCCGATCACTCGGCCACCGCGATGGCGGACGCGCTTAAC 321	262 ATCACCGC
IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100	81 IleThral
GTCCAACGCGTGGTGGGGGCGCCCGCGGCGCAGTCTCGGCATCTCCGCCGCCGCGGCGTG 261	202 GTCCAACG
ValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVal 80	61 ValGlnAr
ATCGGCCTACCGCCTTCCTCGGCTTGGGTGTTGTCGACAACGGCAACGGCGCACGA 201	142 ATCGGGC
IleGlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArg 60	41 IleglyPr
GGGCAGGCGATGGCGATCGCGGGCCAGATCCGGTGGGGGGGG	82 GGCAGGC
GlyGlnalaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40	21 GlyGlnAl
	22 ACGGCCGC
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Search completed: September 5, 2003, 09:04:16 Job time : 264.595 secs

us-09-684-215a-4.rst

## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 5, 2003, 08:27:24 ; Search time 2280.41 Seconds

(without alignments)

1406.846 Million cell updates/sec

Title:

US-09-684-215A-4

Perfect score: 675
Sequence:

1 TRASDNFQLSQCGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 132
Scoring table: BLOSUM62
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Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Xgapop 10.0, Xgapext Ygapop 10.0, Ygapext Fgapop 6.0, Fgapext Delop 6.0, Delext Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Listing first 45 summaries

Command line parameters:
-WODEL-Frame+ p2n.model -DEV=xlp
-Q=/cgn12_1/USPTO_sp001_p/US09684215/runat_05092003_072202_572/app_query.fasta_1.853
-DB=EST -QFMY=fastap -GUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_ECORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15 -MODE=LOCAL
-OUTFMY=pcto -NORM=ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-2000000000
-USER=US09684215_GCGN_1 1_4575_Grunat_05092003_072202_572 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEC_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV_TIMEOUT-120 -WARN TIMEOUT-30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7
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EST: \*

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em\_gss\_pro:\* em\_gss\_rod:\* em\_gss\_phg:\* em\_gss\_mam:\* em\_gss\_vrl:\* gb\_gssl:\* em\_gss\_fun:, em\_gss\_mus: em\_gss\_pln: gb\_est4:\* gb\_est5:\* em\_estfun:\* em\_gss\_vrt: em\_gss\_hum em\_gss\_inv em\_esthum:\* em\_estro:\* em\_htc:\* em\_estmu:\* em\_estov:\* em\_estba:\* em\_estom: em\_estin:\* em\_estpl:\* gb\_est2: gb\_htc:\* gb\_est3: qb\_estl:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

RESULT 1

	U82114 289 bp DNA linear GSS 16-FEB-2001	U82114 ordered cosmid library Mycobacterium leprae genomic clone	cosmid L-373; contig 64, genomic survey sequence.	U82114	U82114.1 GI:3647212	GSS.	Mycobacterium leprae	Mycobacterium leprae	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	Corynebacterineae; Mycobacteriaceae; Mycobacterium.	1 (bases 1 to 289)	
U82114	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	

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US-09-684-215A-4 (1-132) x BH770798
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Silbaq,F.S., Cho,S.N., Cole,S.T. and Brennan,P.J.
Characterization of a 34-kilodalton protein of Mycobacterium leprae
that is isologous to the immunodominant 34-kilodalton antigen of
Mycobacterium paratuberculosis
Infect. Immun. 66 (11), 5576-5579 (1998)
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                                                                                                               Microbiology
Colorado State University
Colorado State University
Colorado State University
Eiglmeier,K., Honore,N., Woods,S.A., Caudron,B. and Cole,S.T. Use
of an ordered cosmid library to deduce the genomic organization of
Mycobacterium leprae. Mol. Microbiol. 7 (2), 197-206 (1993)
Class: unknown.
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LLMGtag541 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.
BH770798
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Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis Sci. Aliments, (2002) In press
Contact: Sorokin A
Genetique Microblenne
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Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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/organism-"Mycobacterium leprae"
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/clone_lib="ordered cosmid library"
? a 83 c 93 g 51 t
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Pseudomonadaceae; Pseudomonas.
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/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGMU2; Site_1: Smal: Library of chromeosmal fragments of L.lactis strain MG1363 was prepared by partial Alu digestion or by sonication."
1 282 c 260 q 458 t
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Domaine de Vilvert, 78352 Jouy
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Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
Email: sorokine@jouy.inra.fr
Class: shotgin
High quality sequence start: 30
High quality sequence stop: 1408.
Location/Qualifiers
ie
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| GTCGCGCTGAACGTCGCCGACCAGTTGAAGAAAGCCGGC-----AAGGTCAGTCGC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 TACGGCCTCGACAAGCCGTCCGGCGCGCTGGTGGCGCAACTGGTGGAAGAAGACGCCCGGCG 157
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Whole-Genome-Sequence variation among multiple isolates of Whole-Genome-Sequence variation among multiple isolates of Psedomonas acruginosa library
J. Bacteriol., (2002) In press
Contact: Chris K. Raymond Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Fax: 2066887344
Email: craymond@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHisIle 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGTCCGCCGACCTGCCGCACCTGGTGGGCAACATGAAGCCGGGCGACAAGATCAACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 GlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsn--------
                                                                                                                                                                                                                                                                                       /clone="pacs1-60_1644"
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                                                                                                                                                                                                                                                                                                                                                    2 others
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Mismatches:
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Matches:
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                                                                                                                                                                                                              1. .959
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                                                                                                                                                                                                                                                                          /db_xref="taxon:287"
                                                                                                                                                                                  Class: shotgun.
Location/Qualifiers
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1. 726

/organism="Oryza sativa (japonica cultivar-group)"
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/clone_lib="osynef"
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XhoI; Uninfected Control"
xhoI; Uninfected Control"
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhaticoideae; Oryzeae; Oryza.

1 (bases 1 to 726)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 ThralaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrp 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 ------GlyGlnIleArgSerGlyGlyGlySerProThrValHisIleGlyPro
                                                                                                                                                                                                                                                                               ΑZ
                                                                                                                                                                                                                          Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerGl,nGlyGlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAla-
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18
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Conservative:
Mismatches:
Indels:
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BACKWARD: gga aac agc tat gac cat g
Plate: 02 row: F column: 19
Seq primer: gga aac agc tat gac cat g.
Location/Qualifiers
                                                                                                                                                                      between rice and Magnaporthe grisea
Unpublished
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120.50
44.03%
30.60%
17.85%
                                                                                                                                                                                                             Contact: Rod Wing
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Qy 15 GlyPheAlaileProlleGlyGlnAlaMetAlaileAlaGly 28	6 GGCTTTGCTATCATCATCATCATAAAATCGCTCCTCAGTTAATTCAGTTCGGA	OY 29 GINITEARGSEFGIYGLYGEFFIOINIYALHISIIEGLYPFOINTAIBFRELEGUGIY 48 ::::::	Qy 49 LeuGlyValValAspAsnAsnGlyAlaArgValGlnArgValUalGlySerAla 68	Qy 69 ProAlaAlaSerLeuGly1leSerThr 77	Oy 78 GlyaspVallientralaValaspGlyalaProlleasnSeralaThralaMetalaasp 97	Qy 98 AlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGly 117	Oy 118 GlyThrargThrGlyAsnValThrLeu 126  Db 333ATCCGGCGAGGCTCAGAAACCTT 356	RESULT 6 AZ934428.	DEFINITION BJ_Ba0002108r B. japonicum BAC library Bradyrhizobium japonicum genomic, genogmic survey sequence.	ACCESSION A293428 VERSION A293428.1 ¢1:13776488 KEYWORDS GS. SOURCE Bradyrhizohim laponicum	Z	REFERENCE 1 (bases 1 to 603) AUTHORS Tomkins, J.P. Wood, T.C., Stacey, M.G., Loh, J.T., Judd, A., Goicoechea	,J.L., Stacew,G., Sadowsky,M.J. and Wing,R.A. TITLE A marker-denge, sequence-ready map of the Bradyrhizobium japonicum genome	JOURNAL Genome Res. 11 (8), 1434-1440 (2001) MEDLINE 21376150 PUBMED 114833585 COMMENT Contact: Wing Da	Comming Common of the Comming Institute Clemson University Clemson University 100 Jordan Hall, Clemson, SC 29634, USA	Tel: 864 656 7288 Fax: 864 656 4293 Email: rwingelemson.edu	FEATURES 1 603	/organism="Bradyrhizobium japonicum" /moi_type="genomic DNA" //stain="USDAIIO" //www.ce="tenomic DNA"	/OB_XREIT=Taxon:3/5" /lab_host="E. col1" /clone_lib="B. japonicum BAC library" /note="Vector: pIndigo536; Site_l: HindIII"  BASE COUNT 109 a 201 c 203 g 90 t ORIGIN	nment Scores:	Fred. No.: U.110 Length: bus Score: 114.00 Matches: 36
Qy 113 GluThrLysSerGlyGlyThrArgThrGlyAsnValThrLeu 126 	SULT 5 925602	N <sub>O</sub>	NON SC	SOURCE SOFGHUM BIGGOOK (SOFGHUM) ORGANISM SOFGHUM bicolor Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD	REFERENCE 1 (Dases 1 to 590) AUTHORS Cordonnier-Pratt,MM., Wentzel,V., Suzuki,Y., Sugano,S., Klein ,R.K., Liang,C., Sun,F., Sullivan,R., Shah,M., Buchanan,C.D., Factors and Draft I	TITLE An EST detabase from Sorghum: ABAl-treated seedlings JOURNAL Unpublished COMMENT Other_ESTs: ABAl_22_F06.gl_A012	Contact: Cordonnier-Pratt MM Laboratory for Genomics and Debuthormatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA	Fax: 706 583 0210 Fmx: 706 583 0210 Email: mmpratt@uga.edu	Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Computer and Disinformation	Jayounting your in the paronatory for genomics and blointoimetres, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to	exclude polyA. Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA) POLYA-Yes.	FEATURES Location/Qualifiers source 1.590	/organism=-sorghum bicolor= /mol_type="mRNA" /cultivar="IS3620C"	/db_xref="taxon:4558" /clone="ABAL_22_F06_A012" /lab_host_B10B-resistant E. coli" /clone llb="Abscisic acid-treated seedling"	/note="Vector: pME18S-FL3; Site_1: Xhoi; Site_2: Xhoi; The library was prepared from polyA+ RNA from seedlings grown in hydroponic culture. After 12 days, medium was	supplemented with 1 mM abscisic acid (ABA), while leaves were misted with a solution of 1 mM ABA. Roots and leaves were harvested after 3, 6, 12, and 24 hr and material from all time points was combined prior to bux isolation	Double-stranded cDNA was cloned unidirectionally into different Drail sites of the PME185-FL3 vector (5-prime Drail site is CACGTGTG, 3-prime Drail site is CACCATGTG	). XhoI excises the cDNA insert." BASE COUNT 136 a 137 c 156 g 161 t ORIGIN	ores: 0.0509 Length: 117.50 Matches: larity: 44.19% Conservative: imlarity: 28.68% Mismatches:	Ouery Match: 17.41% Indels: 29  DB: 14 Gaps: 4	US-09-684-215A-4 (1-132) x CB925602 (1-590)

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Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Restrepo, S., Griffiths, H., van der Hoeven, R., Tsai, J. and
                                                                                                                                          85 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 CGTGCGATCGTGAAGCTTAACGTGCTGCACAG---GGCCAGGACAATGTCGTGAACCTC 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URE:
http://genome_arizona.edu/orders/
                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                               84
                                                                                                                    13 GlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArgSer 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation of a set of potato cDNA clones for microarray analyses
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                                                                                                                                                                                                                                                                                                                          65 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                         105 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
                                                                                                                                                                                                                       305 AAGGGTTCGGTCAGCCGCGCTGGATCGGCGTGATTCAGCCGGTGACG-----
   17
57
12
4
   Conservative:
                 Mismatches:
Indels:
Gaps:
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                                                                                  US-09-684-215A-4 (1-132) x AZ934428 (1-603)
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1. .758
                                                                                                                                                                                                                                                         49 LeuGlyValValAspAsnAsnGly-
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Solanum tuberosum
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BQ514888.1 GI:21373757
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Other_ESTs; EST622302
 43.44%
29.51%
16.89%
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593 ACCCTC 598
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Percent Similarity:
Best Local Similarity:
                                Query Match:
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microarray analyses mixed potato cissues.

//oce="Vector: pBluescript SN(-); Site_1: EcoRI; Site_2:
Xhof: supplier: Combination of untreated and Phytophthora
infestans-treated libraries of stolons, leaves, leaflets,
axillary buds of stem explants, petioles, germinating eyes
, tubers, or roots."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pacs2-164_3239.y3 pacs2-164 Pseudomonas aeruginosa genomic clone pacs2-164_3239, genomic survey sequence.
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Psedomonas aeruginosa library
J. Bacteriol., (2002) In press
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Conservative:
Mismatches:
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1 (bases 1 to 1033)
Spencer, D. H., Raymond, C. K., Smith, E.E.,
Burns, J. L., Kaul, R. and Olsen, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
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Email: craymond@u.washington.edu
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Contact: Chris K. Raymond
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Pseudomonas aeruginosa
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16.74%
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Best Local Similarity:
Query Match:
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BZ561390/c
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Bradyrhizoblaceae; Bradyrhizoblum.
1 (bases 1 to 719)
Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A., Goicoechea,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A.
A marker-dense, sequence-ready map of the Bradyrhizoblum japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A2933900 719 bp DNA linear GSS 24-APR-2001
BAC Library Bradyrhizobium japonicum genomic, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGCGTGGTGATCCAGGAAGTGAACAAGGATCTCGCCGAGTCCTTCGGCCTC----
                               /db_xref="taxon:287"
/clone="pacs2-164_339"
/clone_line="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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Mismatches:
Indels:
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
                                                                                                              236 t
                                                                                                                                                                             Length:
Matches:
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/mol_type="genomic DNA"
/strain="2-164"
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Bradyrhizobium japonicum
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Best Local Similarity:
Query Match:
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                                                                                                           SASE COUNT
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pacs1-60_1644.s1 pacs1-60 Pseudomonas aeruginosa genomic clone pacs1-60_1644, genomic survey sequence.
B2549047.1 G1:27152628
GSS.
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Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 947)
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                                                                                                                                                                                                                                                                                                                                                                                                                          13 GlyGlnGlyPheAlaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleArgSer
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                                                                                                                Fax: 864 656 4255
Email: rwing@clemson.edu
Class: BAC ends
High quality sequence stop: 671.
Location/Qualifiers
1. 719
/organism="Bradyrhizobium japonicum"
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62
25
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Mismatches:
Indels:
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Matches:
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Contact: Chris K. Raymond
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103.50
37.86%
24.29%
15.33%
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Best Local Similarity:
Query Match:
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AJ558965 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018_1_09_a08, mRNA sequence.
AJ558965.1 GI:31661537
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
152 c 159 g 202 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 AAAG%GGGTGATATCATTACCAGCGTCAATAACAAACCCGGTATTTCTGCGGGGTGAAACA 478
                                Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Famil: bassfr@bath.ac.uk
This is one of 2.122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 SerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMet 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 TCATTCGATAAAAGTGAAAATGGTGAAACGCCCAGAAGGGTTGGGGTTCGCTATTCCGACT
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                                                                                                                                                                                                                                                                                      1. 726
/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/clone="PLG00025"
/doc_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 AlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThr 111
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Mismatches:
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Antirrhinum majus (snapdragon)
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Seq primer: M13 Forward
Class: shotgun.
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46.55%
33.62%
15.26%
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Best Local Similarity:
Query Match:
DB:
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10919786
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ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Enterobacteriaceae; Photorhabdus.
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726 bp UNA LILUCAL COLORD POLOTAND STRAIN WI4 WI3 library Photorhabdus luminescens genomic clone PLG00025, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 GGTGGCCTGCAGGTGGGCGATGTGATCAACAGCCTGAACGGCCAGTCGATCAACGAGTCC
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                                                                                                                                                                                                                                                                          Whole genomic shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 GlnAlaMetAlaIleAlaGlyGlnIleArgSer------
                                                                                                                                                                  aeruginosa"
                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                          /organism="Pseudomonas aerugino
/mol_type="genomic DNA"
/strain=1-60"
/db_xref="taxon:287"
/clone="pacs1-60_1644"
/clone=lb="pacs1-60"
/note="clinical isolate 1-60 Wh
               University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 206216954
Fax: 2066857246
Email: craymond@u.washington.edu
Class: shotgun.
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AQ989479.1 GI:9648073
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
1 (bases 1 to 859)
NIH-MGC http://mgc.ncl.nih.gov/.
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              Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamlids; Lamlales; Antirrhinaceae; Antirrhineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 IleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAspValIle 108
                                                                       1 (bases 1 to 765)
2achgo,S., Stueber,K., Saedler,H., Sommer,H. and Schwarz-Sommer,Z.
Antirrhinum EST collection
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AGENCOURT_10739220 NCI_CGAP_ZEMb2 Danio rerio cDNA clone IMAGE:6789351 5', mRNA sequence.
                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:4151"
/clone="0181_109_408"
/clone_1type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
141 c 174 g 229 t
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Mismatches:
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MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany
Location/Qualifiers
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Antirrhinum majus
Eukaryota; Viridiplantae;
                                                                                                                                       Schwarz-Sommer
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Danio rerio
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40.83%
28.33%
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                                                            Antirrhinum.
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AIS97611 423 bp mRNA linear EST 21-APR-1999 tn15f02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167707 3' similar to TR:008664 008664 BCL7C MRNA. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 GlyProThrAlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GlnArgValValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       692 CCTCTCAGCTGTGGTGAAGCTGTAGCCTCTCTCGGTCAGGATCTTCATGAGGTAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         þ
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished \frac{1}{2}
                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbg-remail.nih.gov
Tissue Procurement: Leonard I. 2on, M.D.
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Blossience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 AlaGlyGlnIleArgSerGlyGlyGlySerProThrValHisIle------
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Mismatches:
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Plate: LLAM14289 row: k column: 14
High quality: sequence stop: 662.
Location/qualiflers
1. 859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Danio rerio"
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Best Local Similarity:
Query Match:
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Page 9

ACCESSION		qa	::::::    ::: :::     ::: :::
SOURCE		ζŏ	103 HisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGly 118
REFERENCE AUTHORS TITLE	Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. 1 (bases 1 to 423) NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NAI:Onal Cancer Institute / National Institute of Nauvological		ThrArgThrGly 122
TOTAL		SULT 15	
COMMENT		BISSUSZU/C LOCUS DEFINITION	BI350520 499 bp mRNA linear EST 26-JUL-2002 fr32b05.yl zebrafish adult brain Danio rerio cDNA clone IMAGE:4955073 5' similar to SW:ACT2_FUGRU P53485 ACTIN, CYTOPLASMIC
	CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.	ACCESSION VERSION	2 ; mrka sequence. BI350520 BI350520.1 GI:15044966
	cDNA Library Arrayed by: Greg Lennon, Ph.D.  DNA Sequencing by: Washington University Genome Sequencing Center  Clone distribution: NCI-CGAP clone distribution information can be	KEYWORDS SOURCE ORGANISM	EST. Danio rerio (zebrafish) Danio rerio
	round through the 1.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbry/image/image.html Seq priner: -40UP from Gibco.		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygli; Neopterygli; Teleostel; Ostariophysl; Cypriniformes : Cvprinidae: Danio.
FEATURES SOUTC		REFERENCE AUTHORS	1 (bases 1 to 499) Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
	/organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606"		,S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
	/clone="IMAGE:2167707" /tissue_type="anaplastic oligodendroglioma"		Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
	/lab_host="DH10B" /clone_lib="NCI_CGAP_Brn25"	TITLE JOURNAL	WashU Zebrafish EST Project 1998 Unpublished
	/note="Organ: brain: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I; Site_2: Eco RI: 1St strand cDNA was primed with a Not I - oliqo(dT) primer [5'	COMMENT	Contact: Stephen L. Johnson Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
	TGTTACCAATCTGAAGTGGGAGCGGCCGCATAGGTTTTTTTT		Tel: 314 286 1800 Fax: 314 286 1810
	adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento		Email: zbrafish@watson.wustl.edu cDNA Library Preparation: John Ngai. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome
BASE COUNT ORIGIN	65 a		Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@qenomesystems.com) and Research Genetics, Huntsville, Alabama
Alignment	Scores:		(web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
Score: Percent Sin	2.31 Length: 99.00 Matches: 0.101 44.35% Conservativ		www.rzpd.de) Seq primer: T7 High quality sequence stop: 301.
Query Match: DB:	: 20.23% Mismatches: 14.67% Indels: 9 Gaps:	FEATURES	
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δ,	ValAspAsnAsnGlyAsnGlyAlaArgValGln 		excision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."
3 :	CCCTGGGCTGCCTCAGGGACAGGTGGCACTGGCTCGCTCAAAACAGGG	BASE COUNT ORIGIN	101 a 156 c 125 g 117 t
op Op	bs ArgvalvaldiyserAlaProAlaAlaSerLeuGiyileSerThrGiyAspValileThr 82     :::::   :::::	ent No.:	Length:
δÿ	83 AlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHis 102	Score: Percent Similarity	97.50 : 39.29%

5.2 3.3 6		lyGlnGlyPheAlaIleProIle 20     :: :: CCAATGGTGATGACCTGTCCGTC 371	lyGlyGlySerProThrValHis 40 	lyLeuGlyValValAspAsnAsn 55 	aArgvalGlnArgvalValGlySerAlaProAlaAlaSerLeuGlyIle 75 	rolleasnSeralaThralaMet 95 ::: :: [1] AAGTCCAGAGGAGGATGGCATG 158	lyAspvalileSerValThrTrp 112          ::::: GTGACACCATCACCATAGTCCAT 98	ThrGlyAsnVal 124           AGCAGGCTGGATGGCAACGTG 38
ty: 27.14% Mismatches: 14.44% Indels: 12.64% Gaps:	US-09-684-215A-4 (1-132) x BI350520 (1-499)	9 LeuserGlnGly	21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValH1S	41 IleGlyProThrAlaPheLeuGlyVelValValAspAsnAsn ::	56 GlyAsnGlyAlaArgValGlnArgValValGlySerAlaProAlaAlaSerLeuGlyIle	76 SerThrGlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMet :::	96 AlaAspAlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrp 112 157 GGGCAGGGCGTAACCCTCGTAGATGGCCAGTGTGGGTGACACCATCACCATAGTCCAT 98	113 GlnThrLysSerGlyGlyThrArgThrGlyAsnVal
imilari	.5A-4 (1	9 Leuse	1 G1yG1       0 AGGCA	1 Ile	56 GlyAs 262	6 SerT}	6 Alaas 7 GGGC	3 GlnTh
Best Local Similarity: Query Match: DB:	US-09-684-21	Qy Db 43	Oy 2 Db 37	Oy 4	Qy 5 Db 26	Oy 7 Db 21	Qy 9 Db 15	Qy 11 Db 9

Search completed: September 5, 2003, 11:54:34 Job time : 2287.41 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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5, 2003, 07:24:34; Search time 58.2414 Seconds (without alignments) 1390.474 Million cell updates/sec
- nucleic search, using frame_plus_p2n model
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OM protein
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148 1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQI 30 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-09-684-215A-17 **BLOSUM62** Title: Perfect score: Sequence: Scoring table:

2552756 segs, 1349719017 residues Searched:

5105512 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:\*

and is derived by analysis of the total score distribution.

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4	148	100.0	396	23	AAL40769	
S	148		399	24	ABS71801	a
91	148	100.0	447	18	AAT91466	
<b>~</b> 0	4 4		444	9 6	AAT91403	Mycobacterium tube
0 0	140	100.0	447	1 6	AAV4430	. cubercuiosis vcobacterium ti
10	. 4	. 00	447	20	AAZ19252	M. tuberculosis an
11	148		447	20	AAZ19040	tuberculosis
12	148	00	447	22	AAS03780	M. tuberculosis DN
13	4	00	447	24	AAD47080	
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16	烎	00	675	22	AAS64132	Human /M. tubercul
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6T	4 .	9 6	0 / o	7 C	ACA59940	Prostate cancer the
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4 C	* <		9770	, c	ACA12098	
26.	148	. 0	861	24	ABK39776	ancoding
27	. 4	000	861	25	ACA12105	Human Ral2S-L985P
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30	4	00	006	24	ABQ92443	Human lung cancer
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35	∢ •	900	915	77	AAS64141	Human /M. tubercul
 	770	100.0	915 015	77	AAH93903 ABI 95512	RA12- P775P-ORF3 CO
* 4.0	7		915	25	ACA59949	ate cancer t
36	. 4	000	945	24	ABK39768	DNA encoding lung
37	148	00.	945	25	ACA12097	Human lung cancer
38	4	00.	945	25	8	Lung cancer therap
39	4	00	1002	24	5	E
40	4	00.	1002	24	707	Mycobacterium tube
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42	148	100.0	1002	24	33	~~
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44	148	٠,	1012	77	225	Z/N-termin
<b>4</b> 0	148	<i>:</i>	CENT	47	ABK69/14	DNA encoding numan

ALIGNMENTS BP ABK39777 stancard; cDNA; 186 21-MAY-2002 (first entry) ABK39777;

RESULT 1 ABK39777

Lung tumour; cancer; T cell; immune response stimulator; DNA encoding Eal2S-L985PEx peptide. cytostatic; gene; ss. 

WO200204514-A2. Homo sapiens. Synthetic.

T cell expansion; CD4; CD8; RA12; gene.

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1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 ACGCCCCCGTCCCGATAACTICCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the presence of a cancer in a patient. A for treating a lung cancer in a patient. The polypeptide is useful for tremoving tumour cells from a biological sample. The polynucleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This sequence encodes a lung tumour associated protein or protein fragment, described in the method of the invention.

Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                               Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;
Mcnabb A, Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                        Novel polynucleotide encoding a lung tumour polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; lung cancer; ss; lung tumour; cytostatic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human His-tagged Ral2S-L985PEx fusion protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 186 BP; 39 A; 61 C; 47 G; 39 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 GGGCAGGCGATGCCGAGGCCAGATC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 1879; 223pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215A-17 (1-30) x ABK39777 (1-186)
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                                                                                 2000US-0614124.
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2000US-0658824.
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                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
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Best Local Similarity:
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                                                                                                                                                                                                             03-MAY-2001;
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                                                                                                                      38-SEP-2000;
                                                                                                                                        26-SEP-2000;
                                                                                                                                                         06-OCT-2000;
                                                                                                                                                                        30-OCT-2000;
                                                                                                     29-AUG-2000;
            17-JAN-2002
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ACA12106
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The invention relates to a polynucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences comprising a sequence selected from any of the 14 sequences comprising a sequence selected from any one of the 18 sequences consisting of at least 20 contiguous residues of S1, sequences consisting of at least 20 contiguous residues of S1, sequences that hybridise to S1, sequences contiguous residues of S1, sequences that hybridise to S1, sequences contiguous residues of S1, sequences that hybridise to S1, sequences contiguous residues of S1, sequences may one of the 4 amino acid sequences mentioned in the sepecification, a sequence encoded by the polynucleotide, on expression vector comprising the polynucleotide of the 4 amino acid sequences mentioned in the coperably linked to an expression vector comprising the polynucleotide by the specifically 90%, identity to a sequence encoded by the polynucleotide, an expression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its carnigen building fragment) that specifically binds to the polynucleotide, comprising the polynucleotide, an oligonucleotide that hybridises to cells specific for a tumour protein (comprising and/or expanding T cells specific for a tumour protein (comprising and/or expanding cells, under conditions to the polynucleotide, protein or antigen-presenting cells, under conditions cells and inhibiting the development of a cancer in a patient with the polynucleotide, protein or antigen presenting cells, and thus compasition for polynucleotide, protein ands cells scalated from a patient with the polynucleotide, protein ands cells are useful in a patient. The protein and cells are useful in a patient. The polynucleotide protein ands cells are useful in a patient. The polynucleotide is useful for treating a cancer in the patient. The polynucleotide is also useful as also useful as a probe or primer for relationed protein and an encoder of a cancer in the patient. The polynu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. An amplified portion of the polynucleotide is useful for isolating a full-length gene from a suitable library. The present sequence encodes a fusion protein of human RAI2 with the protein product of a cDNA (full length, extended or partial) isolated from a library derived from lung tumour/cancer cells. Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel lung cancer polynucleotide encoding lung cancer protein, useful for detecting the presence of lung cancer in a patient, and in pharmaceutical compositions, e.g. vaccines, for treating lung cancer
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sapiens.
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                                        Synthetic
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Example 10; SEQID NO 1879; 82pp; English.
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AAL40769
   \mathbb{Z} \times \mathbb{C} \times 
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Bangur CS, Mcnabb A;
of the printed specification, but was obtained in electronic format directly from the USPTO
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gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lung cancer therapyand diagnosis associated cDNA #1767.
                                                                 at segdata.uspto.gov/seguence.html?DocId=20020197669
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                                                                                                                               Sequence 186 BP; 39 A; 61 C; 47 G; 39 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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Vedvick TS,
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Fanger GR,
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Best Local Similarity:
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10-APR-2000;
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30-DEC-1999;
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The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis; vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein; immunogen; cytokine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                20
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                                                                                                                                                                                                                                                                                                                                                                                                                              186
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                                                                                                                                                          Sequence 186 BP; 39 A; 61 C; 47 G; 39 T; 0 other;
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Matches:
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P-PSDB; AA022138.
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                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 kba C-terminal fragment of serine protease antigen MTB2A of Mycobacterium tuberculosis, and a heterologus polynucleotide sequence.

The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the individual is infected with it. The fusion polypeptides are useful as sources of proteins for monitoring binding of serum antibodies to fusion proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 396 BP; 68 A; 132 C; 134 G; 62 T; 0 other;
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Conservative: Mismatches: Indels: Length: Matches: Gaps: 7.59e-15 148.00 100.00% 100.00% 100.00% Best Local Similarity: Query Match: Percent Similarity: Alignment Scores: Pred. No.: Score:

US-09-684-215A-17 (1-30) x AAL40769 (1-396)

1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20 21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30 61 GGGCAGGCGATGGCGATCGCGGGCCAGATC 90 RESULT οp à à g

ABS71801 standard; DNA; 399 BP 02-DEC-2002 ABS71801; 

Human DNA encoding a mammaglobin/RA12 fusion protein. (first entry)

Human; epitope; mammaglobin; breast cancer; cytostatic; T cell; CD4+; CD8+; antigen; RA12; ds; gene.

Chimeric - Homo sapiens. Chimeric - Mycobacterium tuberculosis.

WO200253017-A2.

11-JUL-2002.

08-JAN-2002; 2002WO-US03057.

08-JAN-2001; 2001US-0757417. 08-NOV-2001; 2001US-0008045.

(CORI-) CORIXA CORP

Fling SP, Foy TM, Clapper JD, Wang A, Johnson JC, Sutherland RA;

McNeill PD;

WPI; 2002-706844/76. P-PSDB; ABG94684.

Novel polypeptides comprise one or more human mammoglobin epitopes and polynucleotides encoding the polypeptides, useful for preventing and treating breast cancers

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The invention relates to an isolated polypeptide (I) comprising 7-30 consecutive amino acid residues of human mammaglobin, where one or more mammaglobin-specific T calls specifically reacts with (I).

Also included are (I) a composition comprising (I), in combination with a physiologically acceptable carrier or immunostimulant; (2) a diagnostic comprising (I) and a detection comprising a reporter group; (3) removing tumour cells from a blological sample, by contacting a conditions and for a time sufficient to permit the removal of cells conditions and for a time sufficient to permit the removal of cells conditions and for a time sufficient to permit the removal of cells conditions and for a line sufficient to opermit the removal of cells conditions and for a population (II), comprising T cells prepared using (I); and (5) a composition (C2) comprising a polynucleotide comprising a sequence encoding human mammaglobin (or variant or tagged with an effinity tag), or a polypeptide comprising a human mammaglobin (or variant or tagged with an effinity tag), in combination with an immunostimulant. The peptide is useful for inhibiting the development of breast cancer in a patient, by incubating CD4<sup>-+</sup> and/or CD8<sup>+</sup> T cells conforted from a patient, by incubating cells to the patient, optioning at least one proliferated T cells to the patient, optionated cell, and thus inhibiting the development of breast cancer in the patient. The compositions and methods are useful for inhibiting the development of breast cancer in the patient. The compositions and methods are useful for inhibiting the development of breast cancer in a patient. The compositions and methods are useful for inhibiting the development of breast cancer in a patient. The compositions and methods are useful for present sequence encodes a human mammaglobin/RA12 fusion protein.
                                                                                                                                                           Claim 20; Page 115; 121pp; English.
\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset{\times}{\times}\overset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300000 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 7.66e-15 148.00 100.008 100.008 Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Score:

Sequence 399 BP; 109 A; 96 C; 92 G; 102 T; 0 other;

US-09-684-215A-17 (1-30) x ABS71801 (1-399)

22 ACGCCCCCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGCAGGATTCCCCATTCCCATC 81 1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle á g

à

RESULT 6 AAT91466

AAT91466 standard; DNA; 447 BP

AAT91466;

07-JAN-1998 (first entry) 

Mycobacterium tuberculosis antigen TbRa12 encoding DNA.

Antigen; immunogen; vaccine; tuberculosis; non specific adjuvant; skin testing; M.tuberculosis; ss.

Mycobacterium tuberculosis

Location/Qualifiers 11..409 /\*tag= a /product= Antigen\_TbRal2

WO9709428-A2

13-MAR-1997.

96WO-US14674.

30-AUG-1996;

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13-MAR-1997
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AAV64450
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                                                                                                                                                                                                                                                                                                                                                                                A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence encodes a specifically claimed M tuberculosis antigen, TBRal2. The immunogenic protein, and fusion proteins containing one or more of the proteins or an effect of the proteins or one of the proteins plus BSAT-6, are useful in vaccines, preferably when formulated with a non-specific adjuvant, to induce an immune response against
                                                                                                                                 New immunogenic polypeptide(s) from Mycobacterium tuberculosis - are useful in vaccines for prevention or treatment of tuberculosis, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; tuberculosis; non specific adjuvant;
                                                                             Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis antigen TbRa12 encoding DNA.
                                                                                                                                                                                                                                                                                                    447
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                                                                              Reed SG,
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                          M.tuberculosis (for treatment or prevention).
                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= Antigen_TbRa12
                                                                             Houghton R,
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11..409
                                                                                                                                                                  Claim 3; Page 50; 168pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     testing; M.tuberculosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
       96US-0680574.
95US-0523436.
95US-0533634.
96US-0620874.
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148.00
100.00%
100.00%
                                                                            Campos-neto A, Dillon DC,
Twardzik DR, Vedvick TH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                             (CORI-) CORIXA CORP.
                                                                                                      WPI; 1997-192903/17.
P-PSDB; AAW32422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen; immunogen;
                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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                                                                                                                                                   for diagnosis
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                01-SEP-1995;
22-SEP-1995;
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                                           05-JUN-1996
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                                   22-MAR-1996
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A new immunogenic polypeptide has been developed comprising an immunogenic part of a soluble Mycobacterium tuberculosis antigen (or its variant differing only in conservative substitutions and/or modifications). The present sequence encodes a specifically claimed M. tuberculosis antigen, TbRa12. The immunogenic polypeptide can be used to diagnose M. tuberculosis infection by forming complexes with specific antibodies in the sample. Fragments of DNA encoding the immunogenic polypeptide can be used as diagnostic primers or probes and agents that bind to the antigen, especially monoclonal antibodies or equivalent polyclonal antibodies, are also used for diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tuberculosis; immunogenic; soluble; antigen; protective immunity; TB; vaccine; pharmaceutical; infection; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                New immunogenic polypeptide(s) from soluble M. tuberculosis antigens - useful for diagnosis of M. tuberculosis infection
                                                                                                                                                                                                                    Skeiky YAW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M. tuberculosis immunogenic polypeptide TbRal2 DNA
                                                                                                                                                                                                                    Reed SG,
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 49-50; 190pp; English.
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                                                          95US-0523435.
95US-0532136.
96US-0620280.
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                                    96US-0680573
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Twardzik DR, Vedvick TH;
  96WO-US14675
                                                                                                                              96US-0658800
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                                                                                                                                                                       CORP.
                                                                                                                                                                                                                                                                              WPI; 1997-192904/17.
P-PSDB; AAW32354.
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Best Local Similarity:
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                                                               01-SEP-1995;
22-SEP-1995;
22-MAR-1996;
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30-AUG-1996;
                                                                                                                              05-JUN-1996;
                                             12-JUL-1996
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Skeiky YAW,
 (CORI-) CORIXA CORP $
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18-FEB-1998;
                                       Campos-Neto
                                                         Reed SG,
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   This sequence encodes an immunogenic portion of a soluble Mycobacterium tuberculosis (MT) antigen which can be used in a method for inducing protective immunity against tuberculosis (TB). This sequence can be formulated into vaccines and/or pharmaceutical compositions for immunising against M. tuberculosis infection or may be used for the
                                                                                                                                                                                                                                            Immunogenic Mycobacterium tuberculosis polypeptide(s) and DNA - use to develop products for the detection of M. tuberculosis infection and for diagnosis, treatment and prevention of tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuberculosis; infection; diagnosis; antigen; TbRa12;
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                                                                                                                                    Lodes MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                  Houghton R, Lodes M
lzik DR, Vedvick TS;
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                                                                                                                                                                                                                                                                                                                   Claim 3; Page 62-63; 230pp; English.
                                                                                                                                                   Twardzik DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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 97WO-US18293.
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96US-0729622
                                   97US-0818112
96US-0730510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosis of tuberculosis,
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                                                                                                                                  Dillon
                                                                                                                                  Campos-Neto A, Dillor
Reed SG, Skeiky YAW,
                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                       WPI; 1998-261042/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                             P-PSDB; AAW81657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 447
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07-OCT-1997;
                                     13-MAR-1997;
                                                       11-OCT-1996;
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11-OCT-1996;
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This DNA sequence codes for Mycobacterium tuberculosis soluble antigen TDRa12 (see MAN64294). It was isolated from a M. tuberculosis strain H37Ra expression library with rabbit anti-ser raised against M. tuberculosis supernatant. The invention relates to compositions and methods for diagnosing tuberculosis. It provides polypeptides (see AAN64291-W64379) comprising an antigenic portion of a soluble M. tuberculosis antigen, or an immunogenic portion of an M. tuberculosis antigen, as well as DNA sequences encoding such polypeptides, recombinant expression vectors and transformed or transfected host cells. Also claimed are methods and diagnostic kits for detecting M. tuberculosis infection in a patient using these polypeptides, antibodies or oligonucleotide probes and primers, for the diagnosis of tuberculosis.
                                                                                                                                                                       New isolated Mycobacterium tuberculosis polypeptides and DNA - used to develop products for the detection of M. tuberculosis infection and diagnosis of tuberculosis
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  DC, Houghton R, Lodes MJ;
Twardzik DR, Vedvick TS;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                       Claim 3; Page 61; 250pp; English.
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98US-0025197
Dilion DC,
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                                                                                  WPI; 1998-251292/22:
P-PSDB; AAW64294.
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WPI; 1999-527416/44.
P-PSDB; AAX38959.
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                                                                                                                                                                                                                                                                                                                               The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. Bor natural killer cells and/or macrophages in tuberculosis-immune subjects. AAX19249 to AAX19460 and AAY39083 to AAX39225 are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen; diagnosis; detection; infection; antibody; immunisation;
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Z, Vedvick TS;
                                                   Houghton R;
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Conservative:
Mismatches:
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Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
                                              Campos-Neto A, Dillon DC, Hendrickson RC, Ho
Lodes MJ, Reed SG, Skeiky YAW, Twardzik DR,
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                                                                                                                                                                                                                                                                                   Claim 3; Page 73; 299pp; English.
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98US-0024753
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                                                                                                                             WPI; 1999-527409/44.
P-PSDB; AAY39096.
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(CORI-) CORIXA CORP.
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18-FEB-1998;
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DB:
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1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
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                                                       This invention describes novel recombinant antigens and their encoding nucleic acids derived from Mycobacterium tuberculosis. The novel polypeptides are useful for detecting M. tuberculosis infection in a biological sample by detecting antibodies which bind with the polypeptides, and are useful as vaccines for immunizing against M. tuberculosis infection. The new detection methods are needed as
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New polypeptide comprising antigenic portions of M. tuberculosis
                                                                                                                                                   current vaccination strategies do not provide 100% immunity
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                                                                                                                                                                              Sequence 447 BP; 79 A; 146 C; 149 G; 72 T; 1 other;
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Matches:
Conservative:
Mismatches:
Indels:
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/product= "TbRa12"
                    Claim(F) Page 103; 323pp; English.
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99US-0158425.
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P-PSDB; AAU01889.
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                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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an M. tuberculosis antigen. Compositions comprising at least
2 heterologous antigens, as a fusion protein, and vectors expressing the
fusion proteins are used as vaccines to prophylactically immunise
mammals (especially humans) against infection by Mycobacteria. The
compositions contain at least 2 heterologous antigens that increase the
serological sensitivity of individuals infected with tuberculosis, a
disease frequently affecting patients with acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                              mammals using fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; immunity; diagnostic agent; gene therapy; Ra12 antigen;
            Vaccinating against Mycobacteria infections in mammals us:
proteins comprising combinations of heterologous antigens
                                                                             sequence encodes Mycobacterium tuberculosis TbRal2,
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/product= "Ra12 antigenic protein"
/note= "No start codon"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                  Example 2; Page 162; 168pp; English.
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11..409
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148.00
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P-PSDB; AAE29705.
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                                                                                                                                                                                                                                                                                      Best Local Similarity:
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                                                                                                                                                                                   disease, AIDS
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide. The recombinant nucleic acid comprises a heterologous polynuclectide sequence encoding an antigen or an antigenia from Mycobacterium sp. and a Leishmania polynuclectide sequence encoding a polypeptide or its fragment. The Leishmania polynuclectide is selected from TSA, LeIF, MIS, and 6H polynuclectides. Sequences of the invention are used in methods for eliciting immune response in mammals. They are useful as vaccines to elicit protective immunity against pathogenic microorganisms such as Leishmania and Mycobacterium tuberculosis. Fusion polypeptides are used for enhancing the expression of polynuclectides, as in vivo diagnostic agents and for raising antibodies in a non-human animal. The invention is used in gene therapy. The present sequence is M. tuberculosis Rall (C-terminus of MTB32A; RA35FL) antigen encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium species MTB32A C-terminal peptide encoding cDNA, MTBRa12.
New recombinant nucleic acid molecule comprising a Leishmania TSA, LeIF, MIS or 6H polymuclectide, useful as vaccine to elicit protective immunity against pathogenic microorganisms e.g. Leishmania and Mycobacterium tubergulosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion protein; antigen; serological sensitivity; immune response; tuberculosis; infection; vaccine; MTB32A; Ra32FL; WTBRa12; ss.
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/product= "Ra35 protein fragment"
/note= "CDS does not include start codon"
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
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                                                                                   Disclosure; Page 83 🖁 155pp; English.
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11..409
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2001US-265737P.
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Best Local Similarity:
Query Match:
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01-FEB-2001;
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The present invention relates to fusion proteins containing at least two Mycobacterium species antigens, nucleotides encoding them and compositions comprising such fusion proteins. The present invention particularly relates to nuclear acids encoding fusion proteins that include two or more individual M. tuberculosis antigens which increase the serological sensitivity of sera from individuals infected with cuberculosis and methods for their use in diagnosis, prevention and treatment of tuberculosis infection. Sequences of the invention and treatment of tuberculosis infection. Sequences of the invention are useful for eliciting an immune response in a mammal, e.g., human, immunised with BCG. They are useful in the diagnosis, treatment and prevention of Mycobacterium infection. The fusion proteins and the polynucleotides are useful as diagnostic tools in patients infected utibodies or cell-mediated immunity against M. tuberculosis, for the diagnosis of an infection or monitoring of disease progression, as immunogens to generate or elicit a protective immune response in a continent and for raising anti-M. tuberculosis antibodies in a non-human animal. Sequences of the invention are also used as vaccines. MTB32A fusion proteins of the invention are useful as in vivo diagnostic agents CDRA, MTBRB12. C-terminal protein fragment (residues 244-355) encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ACGCCCCCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCCCCATTCCCGATC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ral2; serine protease antigen; MTB32A; Mycobacterium tuberculosis;
vaccine; eukaryotic; prokaryotic origin; serum antibody; fusion protein;
Immunogen; cytokine; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                         Composition comprising MTB39 antigen and MTB32A antigen from Mycobacterium species, useful for eliciting immune response in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence encoding Ral2-mammaglobin fusion protein.
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                     Disclosure; Page 99; 136pp; English.
                   Alderson M;
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148.00
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Chimeric - Unidentified.
                                                    WPI; 2002-147798/19
                   Reed S,
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                                                                          P-PSDB; AAE17569
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                   Skeiky Y,
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The invention relates to a recombinant nucleic acid molecule encoding a fusion polypeptide, comprising a polynucleotide sequence of Ral2, a 14 to Ra C-terminal fragment of serine protease antigen Whal3A of Mycobacterium tuberculosis, and a heterologous polynucleotide sequence. The recombinant fusion nucleic acids and polypeptides are useful for providing stable and high yield expression of fusion polypeptides of both eukaryotic and prokaryotic origin and to encode a protein product for use as an antigen for detecting serum antibodies. The presence of serum antibodies to M. tuberculosis antigens in an individual indicates that the influences of proteins and as an immunogen to induce and/or enhance immune responses. The coding sequences can be ligated with a coding sequence of another molecule such as M. tuberculosis antigens, a cytokine or an adjuvant and can be used in vivo as a DNA vaccine. This polynucleotide sequence
                                                                                                                                                                                                                                                                                                                           Recombinant nucleic acid molecule for producing high yield expression of desired fusion polypeptides, encodes fusion polypeptide comprising Mycobacterium tuberculosis coding sequence and heterologous polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 ACGCCCCCCCCCTTCCACCTTCCACCTCTCCCAGGGTGGGCAGGATTCGCCATTCCCATC
                                /product= "Ral2-mammaglobin fusion protein"
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Job time: 59.5747 secs
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                                                                   WO200125401-A2
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Location/Qualifiers

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Scoring table:

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Perfect score:

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APPLICANT: DILLOW, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: Pusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
FILE REFERENCE: 014058-009020US
FILE REFERENCE: 1999-04-07
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-03-13
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
sequence 15, Appl sequence 1, Appl sequence 1, Appl sequence 1, Appl sequence 1, Appl sequence 17, Appl sequence 17, Appl sequence 182, App sequence 822, App sequence 822, App sequence 1862, App sequence 1862, App sequence 1862, App sequence 353, App sequence 353, App sequence 353, App sequence 344, App sequence 834, App sequence 1861, App sequence 351, App sequence 1864, App sequence 351, App sequence 1864, App sequence 388, App
                0.S-09-287-849-1
2 US-10-384-849-1
2 US-10-193-002-44
2 US-10-193-002-17
2 US-09-895-814-892
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3 US-09-895-91-862
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US-09-938-864-388
US-10-025-380-1084
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US-10-002-603-388
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Skeiky, Yasir A.W.
Dillon, Davin C.
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1584.308 Million cell updates/sec
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    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published_Applications_NA:*
                                                                                                                                                                                                                                                                                        Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq length: 0 seq length: 2000000000
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Match Length DB
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Percent Similarity:
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NAME/KEY: CDS
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                                                                                                                                                                                                                                               SEQ ID NO 27
LENGTH: 702
                                                                                                                                                                                                                                                                           TYPE: DNA
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens' of Mycobacterium tuberculosis Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                               21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
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                                                                                                       OTHER INFORMATION: Description of Artificial Sequence:bi-fusion OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading OTHER INFORMATION: frame 1
NAME/KEY: CDS
LOCATION: (1)..(693)
OTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24), OTHER INFORMATION: reading frame 1
NAME/KEY: CDS
OTHER INFORMATION: reading frame 2
OTHER INFORMATION: reading frame 2
NAME/KEY: CDS
OTHER INFORMATION: reading fiame 2
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                      COTHER INFORMATION: reading frame US-09-287-849-27
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
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                                          SEQ ID NO 27
LENGTH: 702
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APPLICANT:
                                                                      TYPE: DNA
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GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(693)
OTHER INFORMATION: b1-fusion protein Ral2-DPPD (designated Mtb24),
OTHER INFORMATION: reading frame 1
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of Artificial Sequence:bi-fusion OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading OTHER INFORMATION: frame 1 FEATURE:
NAME/KEY: CDS
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Matches:
Conservative:
Mismatches:
Indels:
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FILE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/10/359,460
CURRENT FILING DATE: 2003-02-05
PRIOR PILING DATE: 1999-04-07
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-03-13
PRIOR PELICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-03-18
PRIOR PLING DATE: 1997-10-01
PRIOR PLING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SED ID NOS: 46
SOFTWARE: PATENTIN VET. 2.1
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; OTHER INFORMATION: reading frame
US-10-359-460-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (2)..(700) OTHER INFORMATION: reading frame
                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens;
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
FILE REFERENCE: 014058-009020US
CURRENT PRILING DATE: 1999-04-07
PRIOR PAPLICATION NUMBER: US 08/818,112
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SEPTRARE: PATENTIN VET. 2.1
                                               910 ATCACCGCGGTCGACGGCGCTCCGATCAACTCGGCCACCGCGATGGCGGACGCGCTTAAC 969
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COTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: Description of Artificial Sequence:tri-fusion OTHER INFORMATION: protein Ral2-TbH9-Ra35 (designated Mtb32-Mtb39 OTHER INFORMATION: puston)
NAME/REY: modified_base
LOCATION: (30)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: modified_base
LOCATION: (33)
OTHER INFORMATION: n = g, a, c or t
NAME/KEY: CDS
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Mismatches:
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NAME/KEY: modified_base
LOCATION: (2270)
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LENGTH: 2287
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325 GGGCATCATCCCGGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCACGCGT 384
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Patent No. US20020164588A1
GENERAL INCOMATION:
APPLICANT: Elsenberg, David
APPLICANT: Elsenberg, David
APPLICANT: Elsenberg, David
APPLICANT: MATCOTTE, MATCOTT
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                                                                            121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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Matches:
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LENGTH: 1068
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LOCATION: (2270)
OTHER INFORMATION: n = g,
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                 NAME/KEY: modified_base
                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                            Alignment Scores:
                                                             US-10-359-460-1
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Fublication No. US2030147911A1

GENERAL INFORMATION:

APPLICANT: Skeiky, Yasiz A.W.

APPLICANT: Skeiky, Yasiz A.W.

APPLICANT: Davin C.

APPLICANT: Dallon, Davin C.

APPLICANT: Alderson, Mark

APPLICANT: Corixa Corporation

TITLE OF INVENTION: and Their Uses

FILE REPERBENC: 01408-009020US

CURRENT APPLICATION NUMBER: US/10/359,460

CURRENT FILING DATE: 1999-04-07

PRIOR PILING DATE: 1999-04-07

PRIOR PILING DATE: 1997-10-01

PRIOR PILING DATE: 1997-10-01

PRIOR APPLICATION NUMBER: US 09/025,197

PRIOR APPLICATION NUMBER: US 09/025,197

PRIOR PILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 09/025,197

PRIOR PILING DATE: 1998-01-18

PRIOR PELICATION NUMBER: US 09/025,304

PRIOR PILING DATE: 1998-12-30

NUMBER OF SEQ ID NOS: 46

SEQ ID NO S: 46

SEQ ID NO S: 46

LENGTH - 2027
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                                                        GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis
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                                                                                                                                                                                                                                                                                                                           ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: n = g,
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LOCATION: (42)
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Skeiky, Yasir A.W.
Skeiky, Yasir A.W.
Steiky, Anton Campos Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twarditk, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: ÎBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                     US-09-684-215A-4 (1-132) x US-10-359-460-1 (1-2287)
                                                                           Matches:
                                                         Length:
                                                                                                                                         Gaps:
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STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Publication No. US2003@143243A1
GENERAL INFORMATION:
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81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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             Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS (TUBERCULOSIS)
                                                                                                                                                             COUNTRY: USA
ZIP: 98104 - 7092
ZIP: 98104 - 7092
COMPUTER READABLE FORM:
MEDIUN TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                             ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEFONS: (206) 622-4900
TELEFONS: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-684-215A-4 (1-132) x US-10-193-002-4 (1-447)
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAX-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/193,002
FILING DATE: 10-Jul-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
Lodes, Michael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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670.00
99.24%
99.24%
                                                                                                                                CITY: Seattle
STATE: Washington
                                                                                 CORRESPONDENCE ADDRESS
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                                                                SEQUENCES:
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Best Local Similarity:
                                                                NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J:
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFA: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
            APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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Dillon, Davin C.
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Vedvick, Thomas S.
Twardzik, Daniel F
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Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                             LENGTH: 447 base pairs
                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                               5.01e-69
670.00
99.24%
99.24%
                                                                PRIOR APPLICATION DATA:
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Best Local Similarity:
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81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 98104 *7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPOTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ŠEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                      121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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REFERENCE/DOCKET NUMBER: 210121.417C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
ATTONNEY/AGENT INFORMATION:
NAME: MAKL, DAVID J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/10/193,002
FILING DATE: 10-JJ1-2002
CLASSIFICATION: <UNFOWN>
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SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skeiky, Yasir A.W.
Dillon, Davin C.
Campos Neto, Antonia
Houghton, Raymond
Vedvisk, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (206) 622-4900
)6) 682-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/10193002
Publication No. US20030135026A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 17
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ADDRESSEE: ŞEED aı
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STATE: Washington
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US-10-193-002-17
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMM
AND DIAGNOSIS OF TUBERCULOSIS
                  ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
                                   Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
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Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                      Sequence 17, Application US/10084843 Publication No. US20030143243A1 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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LENGTH: 1872 base pairs
                                                                                                                                                                           APPLICANT: Reed, Steven G.
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STRANDEDNESS: single
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STATE: Washington
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Best Local Similarity:
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Percent Similarity:
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  Alignment Scores:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
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                                  Conservative:
Mismatches:
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            Length: Matches:
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Patent No. US20020022248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Wang, Aijun
Skeiky, Yasir A.W.
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670.00
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US-09-759-143-822
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                             Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-759-143-822
Alignment Scores:
Pred. No.:
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GlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArg 120
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APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymonian D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210111.427024
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
  675
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                                      Conservative:
Mismatches:
Indels:
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  Length:
Matches:
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Patent No. US20020051977A1
GENERAL INFORMATION:
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Jiang, Yuqui
Henčerson, Robert A.
Kalcs, Michael D.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Skeiky, Yasir A.W.
Hepler, William
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Vedvick, Thomas S.
Carter, Darrick
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Retter, Marc W.
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81 IleThralaValaspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR 1
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.53462
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Matches:
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SOFTWARE: FastSEQ for Windows Version 3.0
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020192763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Jiang, Yuqiu APPLICANT: Kalos, Mitchael D. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Vadvick, Thomas S. APPLICANT: Vadvick, Thomas S. APPLICANT: Carter, Darrick
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Hepler, William T.
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US-09-895-793-822
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US-09-895-793-822
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LENGTH: 675
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 21012.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ. ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ. ID NO 822
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Conservative:
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Patent No. US20020081680A1
GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: HOMC
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                                                          Alignment Scores:
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81 IleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
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CURRENT APPLICATION UNBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
SOFTWARE: FASISEQ for Windows Version 3.0
SEQ ID NO 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ThrGlyAsnValThrLeuAlaGluGlyProProAla 132
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                 Conservative:
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                                 Mismatches:
Indels:
Matches:
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Houghton, Raymond L.
Vinals y de Bassols, Carlota
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; Publication No. CS20030157089A1
; GENERAL INFORMATION:
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Watanabe, Yoshihiro
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Hepler, William T.
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Vedvick, Thomas S.
Carter, Darrick
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer
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                                                                                                                  21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                 1 ThralaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
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APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Susan L.
APPLICANT: Raios, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carig H.
APPLICANT: Carig H.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Mang, Aljun
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Houghton, Robert A.
APPLICANT: Houghton, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DARE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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CORGANISM: Homo sapiens
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SEQ ID NO 822
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; LENGTH: 675 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-144-678A-822

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81 IleThralaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsn 100
                                                                                                                                                                                                                                     82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAG------CTTCCCACCGTTCAT 129
                                                                                  21 GlyGlnAlaMetAlaIleAlaGlyGlnIleArgSerGlyGlyGlySerProThrValHis 40
                                                                                                                                                                                           80
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Mismatches:
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Search completed: September 5, 2003, 12:04:43 Job time : 196.961 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - nucleic search, using frame\_plus\_p2n model September Run on:

(without alignments)
1390.474 Million cell updates/sec 5, 2003, 07:24:34 ; Search time 248.497 Seconds

US-09-684-215A-18 653 1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 128 Title:

**BLOSUM62** Perfect score: Sequence: Scoring table:

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

2552756 seqs, 1349719017 residues Searched:

5105512 of hits satisfying chosen parameters: Total number

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

-WODEL-frame+\_p2n.model -DEV-xlp -Q-CQ012\_1/USPTO\_zppO\_p/US09684215/runat\_05092003\_072201\_548/app\_query.fasta\_1.853 -Q-CQ012\_1/USPTO\_zppO\_p\_D/US09684215/runat\_05092003\_072201\_548/app\_query.fasta\_1.853 -LOSPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST-45 -DOCALIGN-200 -THR\_SCORE=-pct -THR\_MAX=100 -THR\_MIN-0 -ALIGN=15 -WODE-LCOAL -OUTFMY=pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-200000000 -USER-US09684215\_@CGN 1\_1\_626\_@runat\_05092003\_072201\_548 -NCPU-6 -ICPU-3 -NO\_MAAP -LARGEQUERY NEC\_2CORES-0 -WAIT -DSPLOCK=100 -LONGLOG -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP=6 -DELEXT-7

Database

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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\* /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA199:

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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT /SIDS1/gcgdata/geneseq/genesegn-emb1/NA2002.DAT:/ /SIDS1/gcgdata/geneseq/genesegn-emb1/NA2003.DAT: Pred..No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

	Description	n /M. tubero	2- P510S-C	Prostate cancer th	Human lung cancer		er	Ral2/C-terminal po Human /M. tubercul	P775	ralz* P//3P-Ork3 c Prostate cancer th	DNA encoding lung	Lung cancer therap	Human lung cancer Ral2/N-terminal po	DNA encoding human	Human colon tumour DNA encoding Ral2-	Ra12-L985	Lung cancer therap Human /M. tubercul	501S-E2 cc	rate (	encoding hum	UNA encoding Chiam Chlamydia trachoma	DNA encoding Chlam	Chlamydia trachoma C ppeumoniae sero	rach	DNA seq	ncoding h	encoding		mydia tracho	state cancer	DNA encoding cniam Chlamydia trachoma	S					in RA12-P510S-C cDNA.	immunostimulant; tumour.		•
	qı	AAS64132 AAH93896	ABL95503	ACA59940	ACA12098	ACA03284 ABK27798	ABQ92443	ABL49257 AAS64141	AAH93905	ABL95512 ACA59949	ABK39768	ACA03283	ABQ92442 ABL49256	ABK69714	ABZ33699 ABK39775	ACA12104	ACA03290 AAS64153	AAH93917	ABL95524 ACA59961	ABK69715	AAH56353 ABL92582	AAH56341	ABL92570	AAH56267	ABL92496			ABL92585		4	BL9	ALIGNMENTS		BP.			fusion protein	cytostatic; i	tuberculosis.	
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I). (II). antibodies to (II), fusion proteins comprising (II), and isolated (I) and the antibodies are also used in the detection of cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. (I) and cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93397 to AAH93944 and AAM01115 to AAM01118 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotide éncoding a prostate-specific protein, diagnosing, monitoring and treating prostate cancer in a for use in vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SL, Jiang Y, Stolk JA, S
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Retter MW,
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                                                                                                                    121 ThrLeuAlaGiuGlyProProAla 128
                                                                                                                                        Ra12-P510S-C construct cDNA sequence.
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Kalos MD, Fanger GR, Day
Wang A, Meagher MJ;
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUL-2001.
                                                                                                                                                                                                                                                                                            04-OCT-2001
                                                                                                                                                        382
                                                                                                                                                                                                                                                            AAH93896;
                                                                                                                                                                                                            AAH93896
                                                                                                                                                                                          RESULT
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                                                                                                                                                        QQ
                                                                                                                                                                                                                            The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding. T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 GCCTTCCTCGGCTTGGGTGTTGTCGACAACAGGCAACGGCGCACGAGTCCAACGCGTG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
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                                                                                                                                                                                                                                                                                                                                                                                                                               New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                              Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                           Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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                                                                                                                  2000US-0570737.
2000US-0593793.
2000US-0605783.
2000US-0636215.
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2000US-0657279.
2000US-0679426.
2000US-0685166.
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                                                  27-MAR-2001; 2001WO-US09919
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P-PSDB; AAU69899.
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Query Match:
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27-JUN-2000; 2
10-AUG-2000; 2
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06-SEP-2000; 2
02-OCT-2000; 2
10-OCT-2000; 2
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10-OCT-2000; 2000US-0685166
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Best Local Similarity:
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             (XUJJ/)
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(FANG/)
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                                                                                                             GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                           AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                    ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                             Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; gene therapy; gene; ss.
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US-09-684-215A-18 (1-128) x AAH93896 (1-675)
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Chimeric - Homo sapiens.
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2000us-0536857.
2000us-0568100.
2000us-0570737.
2000us-0593793.
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9705-0904804.
9805-0030607.
9805-0115453.
9805-0159812.
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99US-0352616.
99US-0439313.
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2000US-0651236.
2000US-0657279.
2000US-0679426.
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13-JUL-1999;
12-NOV-1999;
18-NOV-1999;
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02-OCT-2000;
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09-MAY-2000;
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09-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention.
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                                                                                                                                                                                                                                               Kalos MI
Carter I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 675 BP; 162 A; 197 C; 190 G; 126 T; 0 other;
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128
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Matches:
Conservative:
Mismatches:
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Gaps:
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653.00
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S I
                                                   JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
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US-09-684-215A-18 (1-128) x ACA59940 (1-675)
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                                                                                        Sequence 675 BP; 162 A; 197 C; 190
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29-AUG-2000; 2000US-0651563
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                                                                                                                                         Percent Similarity:
Best Local Similarity:
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Synthetic.
                                                                                                             Alignment Scores:
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ABK39769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and
                                                                                                                                       Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen;
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Carter D;
Hural J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on DC, Mitcham JL, Harlocker SL, Jiang Y, Retter MW, Stolk JA, Day CH, Vedvick TS, J A, Skeiky YAW, Hepler WT, Henderson RA, Houghton RL, Y De Bassols CV, Foy TM:
                                                                                                                     Prostate cancer therapy associated cDNA #647
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PD, Houghton RL, Y De Bassols CV,
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ThrLeuAlaGluGlyProProAla 128
          ACA59940 standard; cDNA; 675
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                                                                                                 (first entry)
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MITCHAM J L.
HARLOCKER S L.
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WANGA.
SKEIKYYAW.
HEPLERWT.
HENDERSONRA.
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HOUGHTON R L.
Y DE BASSOLS C
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KALOS M D.
FANGER G R.
RETTER M W.
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DAY C H.
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Mcneill PD,
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121
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101 GlyAspVall¶eSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent of fice a displacement of the sequence. Althalphocide of the sequence of the sequence of the sequence. The sequence of the sequence 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Thralaalas@raspasnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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381

261

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201

141 9

382 ACATTGGCCGAGGGACCCCCGGCC 405

ACA12098 standard; cDNA; 822

(first entry)

06-JUN-2003

ACA12098;

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ACA12098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for stimulating and control of a cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynuclectide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for tremoving tumour cells from a biological sample. The polynuclectide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This sequence encodes a lung tumour associated protein or protein fragment, described in the method of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle
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                                                                                                                                                                           Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;
Mcnabb A, Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide encoding a lung tumour polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein
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2000US-0671325.
2000US-0677419.
2000US-0702705.
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                  06-0CT-2000; 2000US-0677419.
30-0CT-2000; 2000US-0702705.
13-DEC-2000; 2000US-0736457.
03-MAY-2001; 2001US-0849626.
                                                                                                                                 (CORI-) CORIXA CORP.
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The invention relates to a polynucleotide encoding a lung tumour protein, comprising a sequence selected from any of the 14 sequences comprising a sequence selected from any of the 14 sequences consisting of at least 20 specification, complement of S1, sequences consisting of at least 20 specification, complement of S1, sequences consisting of at least 20 contiguous residues of S1, sequences that hybridise to S1, sequences consisting of at least 20 contiguous residues of S1, sequences that hybridise to S1, sequences consisting of at least 20 contiguous residues of S1, sequences that hybridise to S1, sequences consisting a sequence of S1. Also included are an isolated applypeptide (comprising the polynucleotide) as expression ontrol sequence encoded by the polynucleotide, on expression control sequence, an isolated antibody (or its the polynucleotide), an expression control sequence, an isolated antibody (or its antigen-binding fragment) that specifically binds to the polypeptide, an oligonucleotide that hybridises to antigen-binding fragment) that specifically binds to the polypeptide, an oligonucleotide that hybridises to comprising the polypeptide, an oligonucleotide that hybridises to comprising the polypeptide, an oligonucleotide that hybridises to the polynucleotide, protein or antigen-presenting colls, under conditions and for a time sufficient to permit the stimulation and/or expansion of the polynucleotide, protein or antigen-presenting cells, and this tender colls isolated from a patient (by incubating CDM++ and/or CDM++ T cells isolated from a patient with the polynucleotide, protein or antigen presenting cells, and thus the patient an effective amount of the proliferate, administering to the polynucleotide, protein and for a cancer in the patient. The patient in the patient of the proliferated of cancer in the patient. The patient in a composition for confiring the development of a cancer in the patient. The patient is an express the coll patient and of a cancer in the patient. The patient is an expr
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                   Human lung cancer protein L801P ORF5/Ra12 fusion protein cDNA
                                                           Human; lung cancer; ss; lung tumour; cytostatic; vaccine;
T cell expansion; CD4; CD8; RA12; gene.
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MCNEILL P D.
CLAPPER J D.
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     patient (particularly lung cancer). The oligonucleotide is useful determining the presence of a cancer in a patient. The protein and cetermining the presence of a cancer in a patient. The protein and coligonucleotides are useful in pharmaceutical compositions, e.g. vaccines. The polynucleotide is also useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. An amplified portion of the polynucleotide is useful for isolating a full-length gene from a suitable library. The present sequence encodes a fusion protein of human RA12 with the protein product of a cDNA (full length, extended or partial) isolated from a library derived from lung tumour/cancer cells. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO.
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  stimulating an immune response in a patient, and for treating a cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polynucleotide associated with the compositions and methods for the therapy and diagnosis of lung cancer.
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Vedvick TS, Bangur CS, Mcnabb A;
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Fanger GR,
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17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated polynucleotide (I) encoding a polypeptide (II) comprising at least a portion of a colon tumour protein. (I). (II) and antibody (III) to (II) are useful for determining the presence of a cancer in a patient. (I). (II) or antigen presenting cells expressing (I) is useful for stimulating and/or expanding T cells specific for a tumour protein, by contacting T cells with (I). (II) or antigen presenting cells that express (I), under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. (II). (II), or antigen presenting cells that express (II) are useful for treating colon cancer in a patient by incubating CD4+ and/or CD8+ T cells. (II). (II), such that T cells proliferate, and administering to the express (II), such that T cells proliferated T cells, thus inhibiting the development of a cancer in the patient. (I) or (II) is useful in vaccines and pharmaceutical compositions for prevention and treatment of colon malignancies and for the diagnosis and monitoring of such
                      cancers. (I), (II) or (III) is useful for detection, diagnosis and/or therapy of human colon cancer. (I) is useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of ribozyme molecules for inhibiting expression of (II) in tumour cells. ABK27564-ABK27807 represent novel human colon cancer coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated polynucleotide encoding a polypeptide comprising a portion of colon tumour protein, useful for detection, diagnosis and therapy of human colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; T cell expansion; tumour; EST; gene; ss; expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sed ID no 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 894 BP; 207 A; 269 C; 237 G; 181 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer expressed sequence tag,
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                                                                                                                              ThrLeuAlaGluGlyProProAla 128
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                                                                                                                                                                                                                                                                                                     BP.
                                                                                                                                                                                                                                                                                                     ABK27798 standard; cDNA; 894
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18-DEC-2000; 2000US-256571P.
10-MAY-2001; 2001US-290240P.
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jiang Y, Hepler WT,
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                                                                                                                                                                                     382
                                                                                                                                                                                                                                                                                                                                                        ABK27798;
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Retter MW, Durham M, Fanger GR, Vedvick TS;
Peckham DW, Cai F, Foy TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as
                                                                                                            1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlyGlyBhealaIleProIle
                                                                                                                                                                                                                      81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                                                                                                                                       22 ACGCCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                           41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                          61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                        21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; lung cancer; lung tumour; cytostatic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lung cancer associated DNA sequence SEQ ID NO:353.
894
128
0
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                        Conservative:
Mismatches:
                                                Indels:
                                                            Gaps:
                                                                                   US-09-684-215A-18 (1-128) x ABK27798 (1-894)
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07-MAY-2001; 2001US-0850716.
28-JUN-2001; 2001US-0897778.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ92443 standard; DNA; 900
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           653.00
100.00%
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PD, Fanger N, R
', Watanabe Y, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-583465/62.
P-PSDB; ABP61920.
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                        Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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McNeill PD,
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                                                Query Match:
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The present invention describes isolated human lung carcinoma polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the bological sample with the oligonucleotide, detecting in the sample, and comparing the amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer.

ABQ92145 to ABQ92486 and ABD61986 to ABD6192 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NO:353.
and as markers to indicate the presence of lung cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; lung tumour; lung cancer; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                           900
128
0
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                                                                                                                                                                                                                                                                                                              Sequence 900 BP; 219 A; 239 C; 246 G; 196 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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                             Page 340-341; 381pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL49257 standard; cDNA; 900
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653.00
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Best Local Similarity:
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   vaccines
                             Claim 8;
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ID ABL
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tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung #tumour proteins, polynucleotides, antibodies, fusion proteins, T gell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes human lung tumour proteins. Human lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                              RA;
                                                                                                                                                                                                                                              Henderson R.
Fanger GR;
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128
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Retter MW, Marnerakis M
Watanabe Y, Peckham DW;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 333-334; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-215A-18 (1-128); x ABL49257
                                                                                                              28-JUN-2000, 2000US*0606421.
02-AUG-2000; 2000US-0630940.
21-AUG-2000; 2000US-0641597.
15-SEP-2000; 2000US*0662786.
09-OCT-2000; 2000US*0685696.
12-DEC-2000; 2000US*073705.
07-MAY-2001; 2001US-0850716.
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653.00
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                                                                                       28-JUN-2001; 2001WO-US21065
                                                                                                                                                                                                                                              Wang A, Skeiky
                                                                                                                                                                                                                                                         McNeill PD, Fanger N,
Vedvick TS, Carter D,
                                                                                                                                                                                                                                                                                               WPI; 2002-090513/12.
                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
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Best Local Similarity:
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                                    WO200200174-A2.
             Homo sapiens.
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                                                                                                                                                                                                                                             Wang T,
McNelll
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81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100

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immune response; ss.

Matches:

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for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human prostate-specific polypeptides and polynucleotides usefuthe diagnosis and treatment of cancer, especially prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalos M
Carter 1
                                                                                                                                                                                                            Human /M. tuberculosis Ra12 fusion protein RA12-P775P-ORF3 cDNA.
                                                                                                                                                                                                                                      Human; prostate cancer; ss; cytostatic; immunostimulant; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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                                                                                                                                                                                                                                                                          - Microbacterium tuberculosis.
                                                 AAS64141 standard; cDNA; 915
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2000US-0651236.
2000US-0657279.
2000US-0679426.
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2000US-0605783.
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                                                                                                                                                                                                                                                                                                                                                                                              2000US-0536857
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                              Chimeric - Homo sapiens
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P-PSDB; AAU69902.
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29-AUG-2000;
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27-JUN-2000;
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12-MAY-2000;
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                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                         AAS64141;
                                                                                                      RESULT 11
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Length:

8.22e-58

Alignment Scores: Pred. No.:

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                                                                                                                         1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                            22 ACGCCCCCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATCGCCATTCCGATC
                                                                                                                                                                                                                                                    81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
                                                                                                                                                                                                          61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SG;
YAW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SL, Jiang Y, Reed
, Stolk JA, Skeiky
128
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         Conservative:
Mismatches:
Indels:
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Retter MW,
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                                                             US-09-684-215A-18 (1-128) x AAS64141 (1-915)
                                                                                                                                                                                                                                                                                                                                     121 ThrLeuAlaGluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 497-498; 543pp; English
                                                                                                                                                                                                                                                                                                                                                                                                  AAH93905 standard; cDNA; 915 BP.
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Kalos MD, Fanger GR, Day CH,
Wang A, Meagher MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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12-JAN-2001;

21-FEB-2002

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present invention describes polynucleotide sequences (I) which encode
          prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and teach be used in vaccine production and gene therapy. (I), (II), and isolated

T cells prepared using (I) or (II) are used treat cancer in a patient.
(I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient.
(I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate ancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 GTCGGGAGCGCTCCGGCGCGAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ral2- P775P-ORF3 construct cDNA sequence SEQ ID NO 834
                                                                                                                                                                                                                     Sequence 915 BP; 167 A; 280 C; 284 G; 184 T; 0 other;
                                                                                                                                                                                                                                                               915
128
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Matches:
Conservative:
Mismatches:
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Chimeric - Homo sapiens.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                      Query Match:
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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                          Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                      Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, 3R, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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                                                                       98US-0115453.
98US-0159812.
99US-0232149.
                                   97US-0806099.
97US-0904804.
98US-0020956.
98US-0030607.
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99US-0352616
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99US-0443686
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FANGER G R.
RETTER M W.
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VEDVICK T S.
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DILLON D C.
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Best Local Similarity:
Query Match:
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WANG A.
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US-09-684-215A-18 (1-128) x ABL95512 (1-915)

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     ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
                  ACGCCCCCGTCCCATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
                              AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro
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                                                                                  ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                                                      Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen;
                                                                                                                                                                                                                                          Prostate cancer therapy associated cDNA #650.
                                                                                                                                                              ThrLeuAlaGluGlyProProAla 128
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                                                                                                                                                                    BP
                                                                                                                                                                                                    ACA59949 standard; cDNA; 915
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04-OCT-2000; 2000US-0679272.
28-MAR-2001; 2001US-0822827.
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HEPLER W T.
HENDERSON R A.
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MITCHAM J L.
HARLOCKER S I
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DAY C H.
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KALOS M D.
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WANG A.
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                                                                                                                                                                                                                      New fusion protein comprising prostate-specific polypeptides, or its immunogenic pcrtions, useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer
                                                                                                                                                                                                                                                                                                                             The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, and particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
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                                                                                           Kalos MD;
Carter D;
Hural J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      part of t
format
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printed specification, but was obtained in electronic form
from the US patent office at
                                                                                         Oillon DC, Mitcham JL, Harlocker SL, Jiang Y, SR, Retter MM, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YW, Hepler WT, Henderson RA, PD, Houghton RL, Y De Bassols CV, Foy TM;
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Matches:
Conservative:
Mismatches:
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MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C
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Best Local Similarity:
Query Match:
DB:
                                                                                           Dillon DC
                                                       FOY T M.
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Pred. No.:
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Mcneill PD,
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                     (HOUG/)
(DBAS/)
(FOYT/)
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ABK39768 standard; cDNA; 945 BP

RESULT 15 ABK39768

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1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the polynucleotide and/or polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for removing tumour cells from a biological sample. The polynucleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This sequence encodes a lung tumour associated protein or protein fragment, described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       printed specification, but was obtained in electronic format directly from WIPO at
                                                            DNA encoding lung tumour protein P801P ORF4 and Ra12 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;
Mcnabb A, Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel polynucleotide encoding a lung tumour polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 did not form part of
                                                                                        Lung tumour; cancer; T cell; immune response stimulator; cytostatic; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; SEQ ID No 1861; 223pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-215A-18 (1-128) x ABK39768 (1-945)
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2000US-0702705.
2000US-0736457.
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                              (first entry)
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P-PSDB; AAU85586.
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06-OCT-2000;
30-OCT-2000;
13-DEC-2000;
                                                                                                                                    Homo sapiens.
Synthetic.
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08-SEP-2000;
                              21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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ABK39768;
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100 261 321 141 201 40 9 80 81 22 ACGCCCGCGT@CGATAACTTCCAGCTGTCCAGGTGGGCAGGATTCGCCATTCGCATC 41 AlaPheLeuGiyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr uGlyProProAla 128 382 ACATTGGCCGAGGGACCCCGGGC 405 142 GCCTTCCTCG 121 ThrLeuAlaGi g g g g à g ò ò õ ö

Search completed: September 5, 2003, 09:04:19 Job time : 250.83 secs Sequence 188, App Sequence 352, App Sequence 336, App Sequence 336, App Sequence 308, App Sequence 308, App Sequence 314, App Sequence 314, App Sequence 316, App Sequence 316, App Sequence 316, App Sequence 316, App Sequence 312, App Sequence 312, App Sequence 312, App Sequence 312, App Sequence 314, App Sequence 314, App Sequence 320, App

e 1, Appli 4, Appli 4, Appli 4, Appli 4, Appli 17, Appl

Sequence

Sequence 4, Sequence 4, Sequence 4, Sequence 17 Sequence 17 Sequence 17

Sequence 17,

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US-09-598-419-188
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US-09-520 412C-352
US-09-520 412C-352
US-09-520 412C-336
US-09-520 412C-336
US-09-520 412C-318
US-09-520 412C-314
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US-09-598-419-312
US-09-598-419-312
US-09-598-419-312
US-09-598-419-320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1862, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
                                                                                                                                                                                                                                                                                                         2148
2287
4403765
4411529
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  Command line parameters:
-MODEL-framet-p2n.model -DEV-xlp
-Q-cgn2_1/USPTO_spool_p/US09684215/runat_05092003_072203_593/app_query.fasta_1.853
-Q-/cgn2_1/USPTO_spool_p/US09684215/runat_05092003_072203_593/app_query.fasta_1.853
-Q-/cgn2_1/USPTO_spool_p/US09684215/runat_05092003_072203_593/app_query.fasta_1.853
-DB-Issued_Patents_NA -OFMT-fastap -SUFFIX-n1 -MINMATCH-0.1 -LOOPCL-0
-LIST-45 -DOCALIGN-200 -THR_SCORES-PCT -THR_MAN-100 -THR_MIN-0 -ALIGN-15
-LIST-45 -DOCALIGN-200 -THR_SCORES-0
-USER-US09684215_CGCN.1_1145_Grunat_05092003_072203_593 -NCPU-6 -ICPU-3
-NO.MARP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPEDCKC+100 -LONGLOG
-DSV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPDP-10 -XGAPEXT-0.5 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
                                                                                                               (without alignments)
825.814 Million cell updates/sec
                                                                                              September 5, 2003, 08:28:59; Search time 68.4138 Seconds
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1 TAASDNFQLSQGGQGFAIPI.....QTKSGGTRTGNVTLAEGPPA 128
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                     OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                           569978 seqs, 220691566 residues
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                    Title:
Perfect sc
Sequence:
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Searched:

APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Marc
APPLICANT: Carter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Retter, Marc
APPLICANT: Fan, Ligun
APPLICANT: Wang, Aljun
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478015
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILLING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0 822 128 0 0 0 Conservative: Mismatches: Indels: Matches: Length: Wang, Tongtong
Bangur, Chaitanya S
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane 1.9e-64 653.00 100.00% 100.00% Homo sapiens Percent Similarity:
Best Local Similarity:
Query Match:
DB: US-09-736-457-1862 SEQ ID NO 1862 LENGTH: 822 Alignment Scores: APPLICANT: APPLICANT: ORGANISM: .. 9 Pred.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

App App App App App App App App

US-09-643-597-1592 US-09-66-421B-353 US-09-736-457-1861 US-09-736-457-1861 US-09-60-421B-351 US-09-620-412C-332 US-09-598-419-332 US-09-556-877-188 US-09-556-877-188 US-09-520-412C-332

822 900 900 1012 1012 11464 11464 11557 11578 11578

6533 6533 6533 6533 6533 6533 6533

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Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence 1862, A Sequence 353, Ap Sequence 353, Ap Sequence 1861, A

Description

US-09-736-457-1862

Length DB

Query Match

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82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
   21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                               82 GGGCGAGGCGATGGCGGTCGCGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
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APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Kan, Liqun
APPLICANT: Angur. Chaitanya S.
APPLICANT: Bangur. Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Logamela X.
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.45509
CURRENT APPLICANTON NUMBER: US/09/606,421B
CURRENT APPLICANTON NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
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Query Match:
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LENGTH: 900
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                                                                                                                                                ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
                                                                                                                                                                                                                          202 GTCGGGAGCGCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC
                                                                                     21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
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APPLICANT: Wang, Tongtong
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Banger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SSOTWARE: FastSEQ for Windows Version 3.0
US-09-684-215A-18 (1-128) x US-09-736-457-1862 (1-822)
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Matches:
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; Patent No. 6426072
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Best Local Similarity:
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LENGTH: 900
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Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120	121 ThrLeuAlaGluGlyProProAla 128	SULT 5 -09-643-597-351	; Sequence 351, Application US/09643597 ; Patent No. 6426072 ; GENERAL INFORMATION ; APPLICANT: Wang, Tongtong	; APPLICANT: Fan, Ligun ; APPLICANT: Kalos, Michael D. ; APPLICANT: Bangur, Chaitanya S. ; APPLICANT: Hosken, Nancy ; APPLICANT: Fanger, Gary R. ; APPLICANT: Lamel X.	APPLICANT: Skelky, Yasir A.W. APPLICANT: Henderson, Robert A. APPLICANT: Henderson, Robert A. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LING CONCER	; FILE REFERENCE: 210121.455011 ; CURRENT APPLICATION NUMBER: US/09/643,597 ; CURRENT FILING DATE: 2000-08-21	; NUMBER OF SEQ ID NOS: 369 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 351 ; LENCTH: 1012	TYPE: DNA ORGANISM: S-09-643-597	Alignment Scores: 2.49e-64 Length: 1012 Score: 653.00 Matches: 128 Percent Similarity: 100.00% Mismatches: 0 Best Local Similarity: 100.00% Mismatches: 0	100.00* 4 Gaps: 128) x US-09-643-597-351 (1-1012)	Oy 1 ThralaalaseraspasnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle 20	Qy 21 GlyGlnalaMetalaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40	41 AlaPheLeuGlyLeuGlyValValAspAsnAshGlyAsnGlyAlaArgValGlnArgVal	Db 187 GCCTTCCTCGGCTTGGGTGTTGTCGACGACGGCGCAACGGCGCACGACGCGTG 246 Oy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80	Db 247 GTCGCGGGCAGCTCCGGCGGCAAGTCTCCGCCACCGGCGACGTGATCACCGCGGGTC 306	307 GACGCGCTCCGATCGCCACCGCGATGGCGACGCGTTAACGGGCATCATCCC	Oy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120	Qy 121 ThrLeuAlaGluGlyProProAla 128
Oy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVallleThrAlaVal 80 	Oy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100	Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120 	Oy 121 ThrLeuAlaGluGlyProProAla 128 	7700	; APPLICANT: Bangur, Chaitanya S. ; APPLICANT: Lodes, Michael A. ; APPLICANT: Fanger, Gary ; APPLICANT: Vedvick, Tom ; APPLICANT: Carter, Darrick	; APPLICANT: Retter, Marc; APPLICANT: Mannion, Jane; APPLICANT: Fan, Liqun	; APPLICANT: Wang, Aljun ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER ; FILE REFERENCE: 210121.478C15	7	SOC TWARE: FASISED LOF WINDOWS VEISION 3.0 SEQ ID NO 1861 TYPE: DNA SORGANISM: Homo sapiens US-09-736-457-1861	2.28e-64 Length: 653.00 Matches:	Best Local Similarity: 100.00% Mismatches: 0 Ouery Match: 100.00% Indels: 0 DB: 4 Gaps: 0	US-09-684-215A-18 (1-128) x US-09-736-457-1861 (1-945) Qy 1 ThralaalaSerAspasnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPhealalleProlle 20	22 ACGCCCGCGTCCGATAACTTCCAGCTGCCCAGGGTGGGCAGGGATTCCCCATTCCGATC	UY 21 GIYGINALAMETALAILEALAGIYGINILELYSLEUFROTHRYAIHISTIEGIYPROTHR 40 	Oy         41 AlaPheLeuGlyLeuGlyValValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60           111111111111111111111111111111111111	61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal	Db 202 GTCGGGAGCGCTCCGGCGAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGGTC 261  Qy 81 AspGlyAlaProIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100	Db 262 GACGCCCCCGATCAACTCGCCCACCGCGATGCCGGACGCCTTAACGGGCATCATCCC 321

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TYPE: DNA ORGANISM: Chlamydia trachomatis
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US-09-598-419-348
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653.00
100.00%
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                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                        US-09-620-412C-348
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LENGTH: 1464
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                                                                                                       Alignment Scores
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Mismatches:
Indels:
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Matches:
ThrLeuAlaGluGlyProProAla 128
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Patent No. 6531315
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Patent No. 6448234
; GENERAL INFORMATION:
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653.00
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                                                         APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
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Best Local Similarity:
                                                   GENERAL INFORMATION:
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81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
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                      FOR TREATMENT AND INFECTION
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APPLICANT: SKelky, Ysair A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIGNOSTS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210111, 469GG
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT APPLICATION NUMBER: US/09/598,419
SOFTWARE FFERENCE: 2000-06-20
NUMBER OF SEO ID NOS: 357
SOFTWARE: FastSEO for Mindows Version 3.0/4.0
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Conservative:
Mismatches:
Indels:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS INVENTION:
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DAME: 72000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FRALSEQ for Windows Version 3.0/4.0
SEQ ID NO 348
LENGTH: 1464
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US-09-598-419-348
US-09-598-419
Sequence 348, Application US/09598419
Patent No. 6565856
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Oy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60	Oy 81 AspGlyalaProIleAsnSeralaThralaMetalaAspAlaLeuAsnGlyHisHisPro 100	Qy 101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120	Qy         121 ThrLeualadluGlyProProAla 128	RESULT 10 US-09-598-419-332 ; Sequence 332, Application US/09598419	GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Skelky, Yasir A.W. APPLICANT: Scholler, John	; TITLE OF INVENTION: COMPOUNDS AND METHOUS FOR TREATMENT AND ; TITLE OF INTENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION ; FILE REFERENCE: 210121.46906 ; CURRENT APPLICATION NUMBER: US/09/598,419	; CURRENT FILING DATE: 2000-06-20 ; NUMBER OF SEQ ID NOS: 357 ; SOFTWARE: FastSEQ for Windows Version 3.0/4.0 ; SEQ ID NO 332	; LENGTH: 155/ ; TYPE: DNA ; ORGANISM: Chlymedia trachomatis US-09-598-419-332	Alignment Scores:     4.4e-64	US-09-684-215A-18 (1-128) x US-09-598-419-332 (1-1557)	Oy 1 ThralaalaSeraspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20	Qy 21 GlyGlnalaMetalaIlealaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40		Oy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspVaII1EThrAlaVal 80		101 GlyaspValileSerValThrTpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
Pred. No.: 4.06e-64 Length: 1464 Score: 653.00 Matches: 128 Bercent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 4 Gaps: 0 US-09-684-215A-18 (1-128) x US-09-598-419-348 (1-1464)	Oy 1 ThralaalaseraspasnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaileProile 20	Oy 21 GlyGlnAlaMetAla11eAlaGlyGlnIleLysLeuProThrValHis1leGlyProThr 40	Oy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60 	Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80 	Qy 81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100	Qy     101 GlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal     120       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 121 ThrLeuAlaGluGlyProProAla 128 · · · · · · · · · · · · · · · · · · ·	RESULT 9 US-09-620-412C-332 ; Sequence 332, Application US/09620412C : Patent NO, 6448334	GENERAL INFORMATION: APPLICANT: Steven P. Fling TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121.46907 CURRENT FILING DATE: 2000-07-20	) NUMBER OF SEQ ID NOS: 363 SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEO ID NO 332	LENGTH: 1557   TYPE: DNA   SOGANISM: Chlymadia trachomatis   Instance of the contract of the	lignment Scores: 4.4e-64 Length:	Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 0	-09-684-215A	Oy 1 ThralaalaSeraspAsnPheGlnLeuSerGlnGlyGlyGlyGhealaileProile 20	Oy 21 GlyGlnalaMetalaIlealaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40 

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Alignment Scores:
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322 GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGGCGCGCGTACAGGGAACGTG 381
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                                                                                APPLICANT: Probst, Peter
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Pling, Steve
Trice of Invention: Compositions and methods for Treatment and
Title of Invention: Compositions of CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: Faster
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Mismatches:
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Matches:
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                    121 ThrLeuAlaGluGlyProProAla 128
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US-09-556-877-188
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Best Local Similarity:
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                                                                           US-09-556-877-188
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LENGTH: 1578
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101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION FILE REFERENCE: 210121, 2000-07-00 CURRENT APPLICATION NUMBER: US/09/620,412C CURRENT FILING DATE: (2000-07-20 NUMBER OF SEQ ID NOS: 363 SOFTWARE: FastSEQ for Windows Version 3.0/4.0 SEQ ID NO 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 188, Application US/09598419
Patent No. 6565856
GENERAL INFORMATION:
APPLICANT: Skelvy, Yasix A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: OCNPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.
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Matches:
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CURRENT FILING DATE: 2000-06-20
WHERE OF SEC ID NOS: 357
SOFTWARE: FASTSEO for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ThrLeuAlaGluGlyProProAla 128
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                                                                                                                                                       TYPE: DNA
ORGANISM: Chlamydia
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Best Local Similarity:
Query Match:
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                                                                                                                                    LENGTH: 1578
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LENGTH: 1578
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GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
   AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
                                                                                                                                                                                                                                                     APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT ATTLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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Mismatches:
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Matches:
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                                                                                                                                                             ; Sequence 352, Application US/09598419; Patent No. 6565856; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Chlamydia trachomatis
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                                                                                                                                                                                                                                                                                                                                                                                   Sequence 352, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.4 649.7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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; ORGANISM: Chlamydia trachomatis
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-MODEL-frame+_p2n.model -DEF-xIP
-MODEL-frame+_p2n.model -DEF-xIP
-Q-/cgn2_1/USPTO_spool_p/US09684215/runat_05092003_072202_559/app_query.fasta_1.853
-Q-/cgn2_1/USPTO_spool_p/US09684215/runat_05092003_072202_559/app_query.fasta_1.853
-Q-/cgn2_1/USPTO_spool_p-VUSO8EP-x=reg -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-b1ts -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORED-P-X - MAX-END-2000000000
-USPR-PCO -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USPR-US0864215_6CGN_1_13962_erunat_05092003_072202_559 -NCPU-6 -ICPU-3
-NO_MAAP -LARGEQUERY -NEG_SCORES-0 -WAIT -DSPBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPDP=10 -XGAPEXT-0.5 -FGAPOP=6
                                                                   5, 2003, 07:52:39; Search time 2285.46 Seconds (without alignments) 2291.192 Million cell updates/sec
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653
1 TAASDNFQLSQGGQGFAIPI......QTKSGGTRTGNVTLAEGPPA 128
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                              nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                      2888711 segs, 20454813386 residues
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Listing first 45 summaries
                                                                                                                                                                                        , Ygapext
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ALIGNMENTS

RESULT 1

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CORTAN   CORPORATION (US)   CORTAN CORPORATION (US)	US-09-684-215A-18 (1-128) x AX201049 (1-675)   Qy	Oy 41 AlaPheLeuGiyLeuGiyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60	Oy 81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100	Qy         121 ThrLeuAlaGluGlyProProAla 128           Db         382 ACATTGGCCGAGGGACCCCGGCC 405           RESULT 3         AX267848           AX267848         675 bp         DNA           LOCUS         AX267848           DEFINITION         Sequence 822 from Patent W00173032.	AX267848 AX267848.1 GI:16516494 Homo sapiens (human) Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,	vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T. and Hendersön,R.A.  TITLE Compositions and methods for the therapy and diagnosis of prostate cancer cancer JOURNAL Patent: WO 0173032-A 822 04-0CT-2001; CORIXA CORPÓRATION (US) FEATURES Location/Qualifiers Source //organism="Homo sapiens" //mol_type="genomic DNA"
AR261272 LOCUS LOCUS LOCUS LOCUS LOCUS AR261272 LOCUS LOCUS AR261272 AR2612	Alignment Scores:     2.28e-44	Oy 1 ThralalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20	Oy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAlaArgValGlnArgVal 60   1111	Qy         81 AspGlyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100           PD         111111111111111111111111111111111111	Qy         121 ThrLeualaGluGlyProProAla 128           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Homo sapiens (human)  ISM Homo sapiens Eukaryota; Metazoa; C Mammalia; Eutheria; P CE 1 Xu,J., Dillon,D.C., M Reed,S.G., Kalos,M.D. Stolk,J.A., Skeiky,Y. Compositions and meth

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PAT 16-FEB-2002
                                                  82 GGGCAGGCGATGGCGATGGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                             22 ACGGCCGCGTCCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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CORIXA CORPORATION (US)
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/mol_type="genomic DNA"
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Wang,T., Bangur,C.S., Lodes,M.J., Fanger,G.R., Vedvick,T.S.,
Carter,D., Retter,M.W., Mannion,J., Fan,L. and Wang,A.
Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                             1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle
                                                                                                                                                          22 ACGCCCCCGTCCCGATAACTTCCAGCTGTCCCAGGGTGGGCCAGGGATTCGCCATTCCGATC
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6509448.
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Location/Qualifiers
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/db_xref="taxon:9606"
197 c 190 g
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                                                                                                                                                                                                                                                                                                                                                                                                                        382 ACATTGGCCGAGGGACCCCCGGCC 405
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Sequence 1862 from patent US
AR277645.
GI:29711294
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281 c 270 g
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1 (bases 1 to 900)
Wang,T., Fan,L., Kalos,M.D., Bangur,C.S., Hosken,N.A., Fanger,G.R., Li,S.X., Wang,A., Skelky,Y.A.W., Henderson,R.A. and McNeill,P.D. Compositions and methods for the therapy and diagnosis of lung
                                                                                                                  26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
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Matches:
Conservative:
Mismatches:
Indels:
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Patent: US 6426072-A 353 30-JUL-2002;
Location/Qualifiers
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                                                            /organism="unknown"
239 c 246 g
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AR220690
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                          ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal
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Matches:
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Mismatches:
Indels:
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CORIXA CORPORATION (US)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
1 269 c 237 g 18:
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Sequence 236 from Patent AX351489
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Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                     82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC 141
 1 (bases 1 to 915)
Mashiki,2. and Harada,J.
Negative pressure control apparatus for engine mounted in vehicle
Patent: US 6321716-A 834 27-NOV-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                           142 GCCTTCCTCGGCTTGGGTGTTGTCGACAACAACGGCAACGGCGCACGAGCGCGTG
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CORIXA CORPORATION (US)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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1 280 c 284 g
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CORIXA CORPORATION (US)
Location/Qualifiers
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1 239 c 246 g 196
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          Sequence 353 from Patent
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                                 AX365960.1 GI:18697458
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Query Match: 100.00% Indels: 0 DB: 6 Gaps: 0	US-09-684-215A-18 (1-128) x AX267860 (1-915)  QY	Qy 21 GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValH1SIleGlyProThr 40	Oy 41 AlaPheLeuGlyCeuGlyValValAspAsnGlyAsnGlyAlaArgValGlnArgVal 60   1111	61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal	Oy 81 AspGlyAlaProlleAsnSerAlaThralaMetAlaAspAlaEeuAsnGlyHisHisPro 100  Db 265 GACGCCGCCACCGCCACCGCGCGCGCGCGCGCTTAACGGGGGGTCATCCCGGGGGGGG	101 GlyAspVallleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal	322 GGTGACGTCGGTGACCTGGCAAACCAAGTCGGCGACGCGTGACAGGGAACGT 121 ThrLeuAlaGluGlyProProAla 128 	382 ACATTGGCCGAGGACCCCCGGCC 403 I 12 644	LOCUS AR277644 945 bp DNA 11near PAT 10-APR-2003 DEFINITION Sequence 1861 from patent US 6509448. ACCESSION AR277644 GI:29711293	KEYWORDS SOURCE SOURCE ORGANISM UNKNOWN.	യയ	JOURNAL Patent: US 6509448-A 1861 21-JAN-2003; FEATURES Location/Qualifiers Source 1. 945	/organism="unknown" BASE COUNT 150 a 318 c 360 g 117 t ORIGIN	11gnment Scores: 3.23e-44 Length:	t Similarity: 100.00% Conservative: 0 cal Similarity: 100.00% Mismatches: 0	100.00% f Gaps: 1-128) x AR277644 (1-945)	AlaSeraspasnPheGl 	GlyGlnalaMetalailealaGlyGlnileLysLeuProthrvalHisileGlyProthr 
ORIGIN Alignment Scores.	Pred No.: 3.12e-44 Length: 915 Score: 653.00 Matches: 128 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Ouery Match: 600.00% Indels: 0	-09-684-215A-18 (1-128) x AX201061 (1-915)	<pre>Qy 1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGlnGlyPheAlaIleProIle 20 11                                   </pre>	Qy 21 GlyGlnalaMetAlaIlealaGlyGlnIleLysLeuProThrValHisIleGlyProThr 40	Oy 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60 	Qy 61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80 	Qy 81 AspClyAlaProlleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100 	Qy       101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnVal 120         111111111111111111111111111111111111	Oy 121 ThrLeualaGluGlyProProala 128 	r 11 360	N N	Σ	REFERENCE 1 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,	of prostat	JOURNAL Patent: WO 0173032-A 834 04-OCT-2001; CORIXA CORPORATION (US)	rce	167	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Fercent Similarity: 100.00% Mismatches: 0 Best Local Similarity: 100.00% Mismatches: 0

Qy         81 AspGlyAlaProIIeAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100           Db         262 GACGGCGTCCCATCACTCGCCCACGCGATGGCGGACGCGCTTAACGGCATCATCCC           Qy         101 GlyAspVall1eSerValThrTrpGlnThrLySSerGlyGlyThrArgThrGlyAsnVal         120           Db         322 GGTGACGTCTCGGTGACCTGGCAAACCAAGTCGGCGCACGCGCACGCGTACAGGGAACGTG         381           Qy         121 ThrLeuAlaGluGlyProFroAla         128           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 14 AR220689 LOCUS AR220689 LOCUS DEFINITION Sequence 351 from patent US 6426072. ACCESSION AR220639 VERSION AR220639 VERSION AR220639 I GI:23327470 KEYWORDS UNKnown. ORGANISM Unclassified. Unclassified. AUTHORS LL,S.X., Wang,T., Kalos,M.D., Bangur,C.S., Hosken,N.A., Fanger,G.R., LL,S.X., Wang,A., Skeiky,Y.A.W., Henderson,R.A. and McNeill,P.D. TITLE Compositions and methods for the therapy and diagnosis of lung Concer JOURNAL Patent: US 6426072-A 351 30-JUL-2002; FEATURES Location/Qualifiers Source Augustanism="unknown" Location/Qualifiers Source Augustanism="unknown" Location/Qualifiers Source Augustanism="unknown" Location/Constitution of the Location of the Location of Loc	IGIN  ignment Scores: 3.47e-44 Length: 1012  ed. No.: 653.00 Matches: 128  ore: 653.00 Conservative: 0  st Local Similarity: 100.00% Mismatches: 0  ery Match: 6 Gaps: 0 Gaps: 09-684-215A-18 (1-128) x AR220689 (1-1012)  1 ThralahaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle	Db   67 ACGCCCCCGTCCCGATAACTTCCAGGGTGGGCAGGGATTCGCCATTCCCATC 126     Qy	Qy         61 ValGlySerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaVal 80           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy         101 GlyAspValIleSerValThrTrpGlnThrLysSerGlyGlyThrargThrGlyAsnVal 120           Db         367 GGTGACGTCATCTCGGTGACCTGGCAAACCAAGTCGGGCGCACGCGTACAGGGAACGTG 426           Qy         121 ThrLeualaGluGlyProProAla 128           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
Qy	10 32 32 38 38	AUTHORS Wang,T., Watanabe,Y., Henderson,R.A., Johnson,J.C., Retter,M.W., Marneakls,M., Carter,D., Fanger,G.R., Vedvick,T.S., Bangur,C.S., Mcnabb,A., Fanger,N., Switzer,A., Wcneill,P.D. and Clapper,J.D.  TITLE Compositions and methods for the therapy and diagnosis of lung cancer JOURNAL Patent: WO 0204514-A 1861 17-JAN-2002; CORIXA CORPORATION (US)  FEATURES Location/Qualifiers Source / Organism-"Homo sapiens" /mol_type-"genomic DNA" /db_xref="taxon:9606" BASE COUNT 150 a 318 c 360 g 117 t		1 ThralaalaSerAspasDisl (1-945)  1 ThralaalaSerAspasDheGlnLeuSerGlnGlyGlyGlnGlyPhealaileProile	OY 41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60  41 AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60  41 AlaPheLeuGlyLeuGlyValValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60  41 AlaPheLeuGlyLeuGlyValValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal 60  41 AlaPheLeuGlyLeuGlyAspAsnAshGrGacGCGCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGG

us-09-684-215a-18.rge

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PAT 15-FEB-2002
                                                                                                                                        Wang,T., Wang,A., Skeiky,Y.A., Li,S.X., Kalos,M.D., Henderson,R.A. Monelli,P.D., Fanger,N., Retter,M., Marneraki,S.M., Fanger,G.R., Vedvick,T.S., Carter,D., Watanabe,Y. and Peckham,D.W. Compositions and methods for the therapy and diagnosis of lung
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CORIXA CORPORATION (US)
Location/Qualifiers
1. 1012
/organism-"Homo sapiens"
/mol_type-"genomic DNA"
/db_xref="taxon:9606"

VT 235 a 289 c 289 g 199 t
              DNA
           AX365958 1012 bp
Sequence 351 from Patent W00200174.
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Search completed: September 5, 2003, 10:31:42 Job time : 2287.8 secs

## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

 nucleic search, using frame\_plus\_p2n model OM protein

5, 2003, 08:27:24; Search time 2211.31 Seconds (without alignments) 1406.846 Million cell updates/sec September

Run on:

Title: Perfect score:

US-09-684-215A-18 653 1 TAASDNFQLSQGGQGFAIPI......QTKSGGTRTGNVTLAEGPPA 128 Sequence:

Scoring table:

0.5 BLOSUM62 Xgappp 10.0, Xgapext Ygappp 10.0, Ygapext Fgappp 6.0, Fgapext Delop 6.0, Delext

45562784 Total number of hits satisfying chosen parameters:

22781392 seqs, 12152238056 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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EST: \* Database :

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em\_estov:\*
em\_estpl:\*
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em\_gss\_inv:\* em\_gss\_pln: em\_qss\_vrt:

em\_gss\_rod:\* em\_gss\_mam: em\_gss\_fun: em\_gss\_pro: em\_gss\_mus

em\_gss\_vrl:\* gb\_gssl:\* em\_gss\_phg:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

U82114 ordered cosmid library Mycobacterium leprae genomic clone cosmid L-373; contig 64, genomic survey sequence. GSS.
Mycobacterium leprae
Mycobacterium leprae
Mycobacteriu; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 289) U82114 U82114.1 GI:3647212 DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE RESULT 1 U82114

REFERENCE

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pacs1-60.1644.s2 pacs1-60 Pseudomonas aeruginosa genomic clone pacs1-60.1644, genomic survey sequence.
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383 ATGGTTGACCTATCTCAATTATCAACAAAGATAGTTCTCAACTGAAATTACCTAGCAGC 324
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                       en Josas cedex, France
                                                                                                                                                                                         /organism="Lactococcus lactis subsp. cremoris"
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/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGMU2; Site_l: Smal; Library of chromosomal fragments of L. lactis strain MG1363 was prepared by partial AluI digestion or by sonication."
282 c 260 g 458 t
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Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 959)
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High quality sequence stop: 1408
Location/Qualiflers
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                   CRJ INRA, Domaine de Vilvert,
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
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Silbaq,F.S., Cho,S.N., Cole,S.T: and Brennan,P.J.
Characterization of a 34-kilodalton protein of Mycobacterium leprae
that is isologous to the immunodominant 34-kilodalton antigen of
Mycobacterium paratuberculosis
Infect. Immun. 66 (11), 5576-5579 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ын/70798 1438 bp DNA linear GSS 01-MAX-2002
LLMGtag541 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.
BH770798
                                                                                                                                                     Colorado State University
Colorado State University
Fort Collins, CO 80523, USA
Eiglmeier.K., Honore.N., Woods,S.A., Caudron,B. and Cole,S.T. Use
an ordered cosmid library to deduce the genomic organization of
Mycobacterium leprae. Mol. Microbiol. 7 (2), 197-206 (1993)
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Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Alients, (2002) In press
Contact: Sorokin A
Genetique Microbienne
                                                                                                                                                                                                                                                                          1. 289
/organism="Mycobacterium leprae"
/mol_type="genomic DNA"
/db_xref="taxon:1769"
/clone="cosmid L-373; contig 64"
/clone="taxon-ref cosmid library"
a 83 9 51 t
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115
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Lactococcus lactis subsp. cremoris
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145.50
58.828
41.188
22.288
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Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastings, M. Burns, J. L., Kaul, R. and Olsen, M. V. Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library J. Bacteriol., (2002) In press Contact: Chris K. Raymond
                                                                                                                                                                                                                               /db_xref="taxon:287"
/clone="pacs1-60_1644"
/clone_lib="pacs1-60"
/note="clinical isolate 1-60 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                2 others
                                                                                                                                                                                              aeruginosa"
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                   Darloure Currers of Washington
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Email: craymond@u.washington.edu
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/organism="Pseudomonas a
/mol_type="genomic DNA"
/strain="1-60"
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Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidaae; Oryzae; Oryza.

1 (bases 1 to 726)
Jantasuriyarat,C., Lu.G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: xhoI; Uninfected Control"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292
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Corganism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                      Unpublished
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, 85721-0088, USA
Tel: 520 628 3967
Fax: 520 621 9288
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                      Email: http://genome.arizona.edu
PCR PRimers
FORWARD: gta aaa cga cga cga gg
BACKWARD: gga aac agc tat gac cat g
Plate: 02 row: F column: 19
Seq primer: gga aac agc tat gac cat g.
Location/Qualifiers
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/dev_stage="3 week"
/lab_host="DH10B"
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122.50
42.868
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Best Local Similarity:
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us-09-684-215a-18.rst

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Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
asterids; lamilds; Solanales; Solanaceae; Solanum.

E. (bases 1 to 758)
Suell.C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
Restrepo,S., Griffiths,H., van der Hoeven,R., Tsal,J. and
Karamycheva,S.A.
Generation of a set of potato cDNA clones for microarray analyses
Unpublished
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute: Orders can be made through URE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ514888 11near EST 07-MAR-2003
EST652303 Generation of a set of potato cDNA clones for microarray
analyses mixed potato tissues Solanum tuberosum cDNA clone STMIO81
3' end, mRNA sequence.
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/note="vector: pBluescript SK(*); Site_l: EcoRI; Site_2:
XhoI; supplier: Combination of untread and Phytophthora infestens-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes
                                                                                                                                                                                                                                                           94 AlaLeuAsnGlyHisHisProGlyAspValIleSerValThrTrpGlnThrLysSerGly 113
                                                                                                                                                                         54 ATTCAGTTCGGAAAAGTTCGTCGTGCTGGCTTGAAT---GTGGACTTCGCTCCGGATCCA 110
                          GlyPhealaIleProIleGlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThr 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 GGTGATATCATCGTTGCAGTGGACGGCAAACCTGTTAAGGGCAAATCTGACCTGCTGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                  74 GlyAspValIleThrAlaValAspGlyAlaProIleAsnSerAlaThrAlaMetAlaAsp
                                                                          6 GGCTTTGCTATTCCATCATCAACTGTACTTAAAATCGCTCCTCAGTTA----
                                                                                                                            35 ValHisIleGlyProThrAlaPheLeuGlyLeuGlyValValAsp-----
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/organism="Solanum tuberosum"
/orlive="mRNA"
/cultivar="Kennebec or Binjte"
/db_xref="taxon:4113"
/clone="STMIOSI"
/tissue_type="mixed tissues"
/lab_host="Sola"
                                                                                                                                                                                                                                                                                                                                65 ProAlaAlaSerLeuGlyIleSer-----
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Seq primer: T7.
Location/Qualifiers
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BQ514888/c
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/cultivar="153620C"
/do_type="mRKRA"
/cultivar="153620C"
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/clone="lb="bascisic acid-treated seedlings"
/clone=lb="bascisic acid-treated seedlings stock to the part of the polyta RNA from seedlings grown in hydroponic culture. After 12 days, medium was supplemented with 1 mM abscisic acid (ABA), while leaves were misted with asolution of 1 mM ABA. Roots and leaves were misted with asolution of 1 mM ABA. Roots and leaves were misted after 3, 6, 12, and 24 hr and material from all time points was combined prior to RNA isolation.
Double-stranded cDNA was cloned undirectionally into different Drail sites of the pME18S-FL3 vector (5-prime Drail site is CACCATGTG
). Xhol excises the CDNA insert."
36 a 137 c .156 g 161 t
                                                                                                  ABAL_22_F06.bl_A012 Abscisic acid-treated seedlings Sorghum bicolor CDNA clone ABAL_22_F06_A012 3', mRNA sequence.
CB925602.1 GI:30161873
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & W University; sequencing done in the Laboratory for Genomics and Bioinformatics, university of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 590)
Cordonnier-Pratt, M.-M., Wentzel, V., Suzuki, Y., Sugano, S., Klein, R., Liang, C., Sun, F., Sullivan, R., Shah, M., Buchanan, C.D.,
Eastman, A. and Pratt, L.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Schences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An EST database from Sorghum: ABA1-treated seedlings Unpublished
110 ThrLysSerGlyGlyThrArgThrGlyAsnValThrLeu 122
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                                               231 AGA------GGCGCTGAATCTCTGGAGGTAACCTTG 202
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Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
POLYA=Yes.
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Indels:
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Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mmpratt@uga.edu
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Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A., Goicoechea
'J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A2934428 603 bp DNA linear GSS 24-APR-2001 BJ_Ba0002108r B. japonicum BAC library Bradyrhizobium japonicum genomic, genomic survey sequence.
A2934428.1 GI:13776488
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                                                                                                                                                                                                                                                                                                             61 ValGlySerAlaProAlaAlaSerLeuGly------
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
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Matches:
Conservative:
Mismatches:
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Gaps:
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Clemson University Genomics Institute
Clemson University
10: Octoban Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/strain="USDA110"
/db_xref="taxon:375"
                                                                                                                                            US-09-684-215A-18 (1-128) x BQ514888 (1-758)
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Location/Qualifiers
roots."
128 g
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Class: BAC ends
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AJ558965 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018_1599.008, mRNA sequence.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamilds, Lamiales, Antirrhinaceae, Antirrhineae,
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Zachgo,S., Stueber,K., Saedler,H., Sommer,H. and Schwarz-Sommer,Z.
Antirthinum EST collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 AAGGGTTCGGTCAGCCGCGGCTGGATCGGCGTGCAGATTCAGCCGGTGACG-
/lab_host="E. coli"
/clone_lib="B. japonicum BAC library"
/note="Vector: pIndigo536; Site_1: HindIII"
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/mol_type="mRNN"
/db_xref="texon:4151"
/clone="018_1_09_a08"
/tissue_type="whole plant"
                                                                                                                                                                                                                                                        Indels:
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Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829,
Location/Qualifiers
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/clone_lib="Antirrhinum majus whole plant" ORIGIN	BASE COUNT ORIGIN	11b 189 a	library." 313 c 292 g
Alignment Scores:  Pred. No.:  Score:  Score:  Al. 24. 48. Conservative: 15  Best Local Similarity: 29.31% Mismatches: 41  Query Match: 15.93% Indels: 46  DB:	Alignment S Pred. No.: Score: Percent Sim Best Local Query Match DB:	cores: ilarity: Similarity: :	11, 92 11,00.50 12,75% 10,43% 15,39%
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Qy 10 SerGinGlyGlyGlyGlyPheAlaileProileGlyGinAlaMetAlaileAlaGlyGin 29 :::	, Vo	4 SerAspAsnP         713 TCCCAGTTTT	SerAspAsnPhedlnLeuSerGlnG 
Oy 30 IleLysLeuProThrValHisIleGlyProThrAlaPheLeuGlyValValNap 49 :::	oy Ob	22 GlnalaMetala 	GlnalaMetalaile-AlaGlyGln    :::   :::        GTCGCGCTGA@CGTTCGCCGACCAG
TCCTGATO	dy do	41 laPheLeuGl :: 605 GTCGCGGCTG	laPheLeuGlyLeuGlyValValAs; :: GTCGCGGCTGGCTGCCCTGGTGAT
Qy 60 ValValGlySerAlaProAlaAlaSerLeuGly	, do	54	GCCTCGACAAGCCGTCCGGCGCGCT
Qy 71IleSerThrGlyAspVallleThrAlaValAspGlyAlaProlleAsnSerAla 88	. KO	68 erLeuGlyIl    :: 485 AGGGTGGCCT	erLeuGlyIleserThrGlyAspVa     ::: AGGGTGGCCTGCAGCTGTGT
Qy 89 ThralametalaaspalaLeuasnGlyHisHisProGlyaspValIIe 104 :::        :::    Db 596 GCCGAGCTATACAAAACACTGGATGAGTATTCCATCGGAGACAAAGTG 643	do D	88 laThrAlaMe :: 425 CCGCCGACCT	laThralaMedalaAspalaLeuAsi
RESULF 9 BZ561390/c	δy	107Th	ThgrpglnThrLysSe
	qa	365 TGATTCGCAA	GGCCAGCGCAAGTC
pacs2-164_3239, genomic survey sequence. BZ561390 BZ561390.1 GI:27181349 GSS Pseudomonas aeruginosa Pseudomonas aeruginosa Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonada	RESULT 10 BZ549047/C LOCUS DEFINITION ACCESSION VERSION	B2549047 pacs1-60_1644.s1 pacs1-60 pacs1-60_1644, genomic su BZ549047.1 GI:27152628	94 .sl pacsl-60 P. genomic surv
Yesudomohadaceads; Pseudomonas. CE 1 (bases 1 to 103) RS Spencer, D. H., Raymond, C. K., Smith, E. E., Sims, E. E., Hastinghall, R. and Olsen, M. V.	KEYWORDS SOURCE ORGANISM	GSS. Pseudomonas Pseudomonas Bacteria; Pr	eruginosa aeruginosa oteobacteria; G
TITLE WAGLE-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library JOURNAL J. Bacteriol., (2002) in press COMMENT Contact: Chris K. Raymond	REFERENCE AUTHORS	Pseudomonada 1 (bases 1 Spencer, D. H. Burns, J. L.,	ceae; Pseudomoneto 947) Raymond, C. K., Kaul, R. and Ols
Genome Center University of Washington Box 352145, Seattle, WA 98105-2145, USA Tel: 2062216954	TITLE JOURNAL COMMENT	Whole-Genome Psedomonas a J. Bacteriol Contact: Chr	Whole-Genome Sequence variate Psedomonas adruginosa libra J. Bacterioli (2002) In p. Contact: Chris K. Raymond
Fax: 2006857244 Email: craymond@u.washington.edu Class: shotgun. FEATURES Source 1. 1033		Genome Cente University o Box 352145, Tel: 2062216 Fax: 2066857	Genome Center University of Washington Box 352145, Seattle, WA 981 Tel: 2062216954 Fax: 2066857244
/organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /strain="2-164" /db xref="taxon:287"	FEATURES	Email: craym Class: shotg Loc	ond@u.washingtor un. tion/Qualifier: \$947
/clone="pacs2-164_3239" /clone_lib="pacs2-164" /note="clinical isolate 2-164 Whole genomic shotgun	)	/or /mo	gantsm="Pseudom Qantspe="genomic gain="1-60"
			gardi a

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47 bp DNA linear GSS 17-DEC-2002 Pseudomonas aeruginosa genomic clone vey sequence.
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::GGTGGCGCAACTGGTGGAAGACGGCCCGGCGGCCA 486
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|::gatcctcaGcctGAAcGGccAGTcGATCAACGAGT 426
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lation among multiple isolates of press
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 726)
ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                               267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Enterobacteriaceae; Photorhabdus.
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Mismatches:
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Department of Biology and Biochemistry
University of Bath
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/db_xref="taxon:287"
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Photorhabdus luminescens
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AQ989479.1 GI:9648073
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AQ989479
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1093)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                       /db_xref="taxon:29488"
/clone="ptG00025"
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected
/note DNA from Strain W14 was size selected
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGENCOURT_10214312 NIH_MGC_107 Homo sapiens cDNA clone IMAGE:6885799 5', mRNA sequence.
BU557763 GI:22908059
EST.
                                                                                                                                                                                     /organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
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Mismatches:
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Acids Res.
Seq primer: M13 Forward
Class: shotgun.
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/organism="Pseudomonas a
/moi_type="genomic DNA"
/strain="MSH"
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                                                       DEFINITION
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                                                                                                                                                                                                              /Mol_type="mRNA"
//db_xxef="taxon:9606"
//clone="INARA"
//db_xxef="taxon:9606"
//clone="INARA"
//db_host="lobalogarcinoma, cell line"
//lab_host="bh10B (phage-resistant)"
//clone_lib="MIH_MGC_lof"
//note="Organ: breast; Vector: poTB7; Site_l: ECORI;
Site_2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."

70 a 416 c 307 g 199 t 100 t 100
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
http://magge.lnl.gov
Plate: LLCM2798 row: f column: 07
High quality sequence stop: 299.
1. 1093
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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790 bp DNA linear GSS 17-DEC-2002 msh2\_5667.x1 msh Pseudomonas aeruginosa genomic clone msh2\_5667, B2577987 |||::: | CTTGCCGCTCCAGGGCACCACGCGCACCAGCAGGAGGAGGTCTCGTCGTTCTTGCC 169 280 ....-GTCATGCCC 412 AlaProileAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisProGlyAsp 102 335 GCGGTAGTGGCCGTGGCTGGCGTCGTGGCGAC-----CGAGGTCAGCACCAGTCGAT 388 ValileSerValThrTrpGlnThrLysSerGlyGlyThrArgThrGlyAsnValThrLeu 122 42 43 LeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgValValGly 62 63 SerAlaProAlaAlaSerLeuGlyIleSerThrGlyAspValIleThrAlaValAspGly 82 --GlnAla 23 Pseudomonas deruginosa Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas. 1 (bases 1 to 790) Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V. Whole-Genome Sequence variation among multiple isolates of Psedomonas agruginosa library J. Bacteriol, (2002) In press 24 MetalaileAlaGlyGlnIleLysLeu---ProThrValHisileGlyProThrAlaPhe 230 GCCGGCCTTGCC-----CACCACCAGGGGGGTCTGGGTGTGCATGCGCGGCTTGGG /db\_xref="taxon:287"
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/clone=lbb=msh"
/note="Environmental isolate. Whole genomic shotgun
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AMZUSS27
LG1_241_G05.g1_A002 Light Grown 1 (LG1) Sorghum bicolor CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Light Grown 1 (LG1)"
/clone_lib="Light Grown 1 (LG1)"
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/seedlings: Vector: Lambda Zap; Site_l: XhoI; Site_2: EcoRI
/ The library was made from poly-A RNA in the cloning
/ The library was made from poly-A RNA in the cloning
/ Prector lambda ZAP II. Clones to be sequenced were
/ Prepared by mass excision."
/ Library RNA in the cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (Dases 1 to 551)
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The University of Genorgia, Department of Plant Biology
The University of Georgia, Department of Plant Biology
That Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
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An EST database from Sorghum: light-grown seedlings
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Mismatches:
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High quality sequence start: 16
High quality sequence stop: 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Sorghum bicolor
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                                                                                                                                                                                                                      AW285527.1 GI:6675371
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Pred. No.:
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/organism="Sorghum bicolor"
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LG1)"
/clone_lib="Light Grown 1 (LG1)"
/clone_lorgan: 10- to 14-day-old light-grown (greenhouse)
/seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI
/relibrary was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
                                                                                                AW285510 546 bp mRNA linear EST 19-JUL-2000 LG1_241_E05.g1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genomics and Bioinformatics
The University of Genomics and Bioinformatics
The University of Genomics and English Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Fax: 706 583 0210
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence
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Sorghum bicolor
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoldeae; Andropogoneae; Sorghum.
(bases 1 to 546)
Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H.
An EST database from Sorghum: light-grown seedlings
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Matches:
Conservative:
Mismatches:
Indels:
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127 c 149 g 149 t
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                                                                                                                                                                                                                                                                                                                                                                               Unpublished
Contact: Cordonnier-Pratt MM
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                                                                                                                                                                                                                    Sorghum bicolor (sorghum)
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AW285510.1 GI:6675354
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LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                          RESULT 14
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Search completed: September 5, 2003, 11:54:41 Job time: 2216.31 secs

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Sequence 822, App Sequence 822, App Sequence 822, App Sequence 1822, App Sequence 1862, App Sequence 1862, App Sequence 353, App Sequence 353, App Sequence 834, App Sequence 834, App Sequence 834, App Sequence 834, App Sequence 1861, App Sequence 351, App Seq
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Sequence 1084, Ap
Sequence 388, App
Sequence 388, App
Sequence 388, App
Sequence 1875, Ap
Sequence 1875, Ap
Sequence 851, App
Sequence 851, App
Sequence 851, App
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427023
                                                                                                                                                                                                                                                                   US-09-850-716A-353
US-09-897-778-353
US-10-117-982-353
US-09-759-143-834
US-09-780-669-834
US-09-822-827-834
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US-09-895-814-834
US-10-144-678A-834
US-10-12-896-834
US-09-736-457-1861
US-09-90-941-1861
US-09-849-626-1861
US-09-849-626-1861
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US-09-897-778-351
US-10-117-982-351
US-09-922-217-1084
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US-09-833-263-1084
US-09-938-864-388
US-10-025-380-1084
US-10-125-635A-388
US-10-002-603-388
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Dillon, Davin C.
Mitcham, Jennifer L.
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Kalos, Michael D.
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 1
US-09-759-143-822
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-MODEL-frame+_pZn.model_-DEV-xlp
-MODEL-frame+_pZn.model_-DEV-xlp
-MODEL-frame+_pZn.model_-DEV-xlp
-WODEL-frame+_pZn.model_-DEVG9684215/runat_05092003_072203_619/app_query.fasta_1.853
-DB-Published_Applications_NA -OEMT-fastap -SUFFIX-rnpb -MINMATCH=0.1
-LOOPCIL-0 'LOOPEXT-0 -UNITS-blts -STRAT-1 -END--1 -MATRIX-blosum62
-LOOPCIL-0 'LOOPEXT-0 -UNITS-blts -STRAT-1 -END--1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFR-TP-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USR-W150864215_GCGN 1_1_130_@runat_05921003_619
-NCPU-6 -ICOPU-3 -NO_MMAP -LARGEQUERY -NG_SCORES-0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT-120 -WARM_IMMEOUT-30 -THREADS-1 -XGAPEXT-0 -SGAPEXT-0.5
-FGAPOP-6 -FGAPEXT-7 -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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                                                                                                                                                                                  (without alignments)
1584.308 Million cell updates/sec
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                                                                                                                                                         5, 2003, 08:54:40 ; Search time 185.821 Seconds
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/ cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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/ cgn2_6/ptodata/1/pubpna/US09_RUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US09_RUBCOMB.seq:*
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  version 5.1.6 - 2003 Compugen Ltd.
                                                                                                          nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1537136 seqs, 1149988732 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Xgapop 10.0 , Xgapext (
Ygapop 10.0 , Ygapext ,
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
     GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                        US-09-684-215A-18
653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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82 GGGCAGGCGATGGCGATCGCGGGCCAGATCAAGCTTCCCACCGTTCATATCGGGCCTACC
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; Sequence 822, Application US/09822827
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangohun
; TITLE OF INVENTION: @OMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE. CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION WUMBER: US/09/822,827
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 822
LENTH: 675
TITLE OF INVENTION: GOMPOSITIONS AND METHODS FOR THE THERAPY ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANGER FILE REFERENCE: 210121/427029 CURRENT APPLICATION NUMBER: US/09/780,669 CURRENT FILING DATE: 2001-02-09 NUMBER OF SEQ ID NOS: 943 SOFTWARE.—FeasUSED for Windows Version 3.0 SEQ ID NO 822
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                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-09-780-669-822
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; ORGANISM: HOMO
US-09-822-827-822
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CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
.NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 675
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Patent No. US20020051977A1
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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McNeill, Patricia
Houghton, Raymond
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Hepler, William
                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Wang, Aijun
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Best Local Similarity:
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APPLICANT: Xu, Jian
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US-09-780-669-822
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CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
          675
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                                Conservative:
Mismatches:
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                      Matches:
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Jiang, Yugiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
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Hepler, William T.
Hencerson, Robert A.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer
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Alignment Scores:
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Mismatches:
Indels:
      TAGNOSIS OF PROSTATE CANCER
             TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CA
FILE REFERENCE: 2012/14/27028
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 11033
SOFTWARE: FastSEQ for Mindows Version 3.0
SOS ID NO 822
LENGTH: 675
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Matches:
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Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Bavin C.
APPLICANT: Mitcham, Sannifer L.
APPLICANT: Harlocken, Susan L.
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William T.
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Vedvick, Thomas S
Carter, Darrick
Li, Samuel X.
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Kalos, Michael
Retter, Marc W
Stolk, John A.
Day, Craig H.
                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-10-144-678A-822
    Deng, Ta
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Hepler, y
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Roll, John A.
APPLICANT: Stolk, John A.
APPLICANT: Udvick, Thomas S.
APPLICANT: Carter, Dav. Craig H.
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Houghton, Raymond L.
Vinals y de Bassols, C
Foy, Teresa M.
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Hepler, William T.
Hural, John
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                                                  ORGANISM: Homo sapiens
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Best Local Similarity:
SOFTWARE: FastSEQ
SEQ ID NO 822
LENGTH: 675
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Wang, Aijun
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                                                                                              THE THERAPY AND
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                                           APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.427627
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF EQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
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Mismatches:
Indels:
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           McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Patent No. US20020168637A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
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Bangur, Chaitanya S.
Lodes, Michael A.
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Mannion, Jane
Fan, Liqun
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US-09-736-457-1862
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LENGTH: 675
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      FOR THE THERAPY AND
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APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Retter, Marc W.
APPLICANT: Marnerakis, Margarita
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
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Matches:
Conservative:
Mismatches:
TITLE OF INVENTION: COMPOSITIONS AND METHODS ITILE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1862
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Patent No. US20020172952A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
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APPLICANT: Watchabe, Yoshihiro
APPLICANT: Watchabe, Yoshihiro
APPLICANT: Watchabe, Yoshihiro
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Ranger, Garter, Darrick
APPLICANT: Fanger, Garter, Thomas S.
APPLICANT: Pangur, Chaltanya S.
APPLICANT: Wodylck, Thomas S.
APPLICANT: Mondab, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2000.10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FASTSEQ for Windows Version 4.0
               Conservative:
Mismatches:
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Publication No. US20030054363A1
GENERAL INFORMATION:
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                Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-10-017-754-1862
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LENGTH: 822
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APPLICANT: Banger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478016
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SOFTWARE: FastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1862
LENGTH: 822
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US-09-902-941-1862
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              GlyGlnAlaMetAlaIleAlaGlyGlnIleLysLeuProThrValHisIleGlyProThr
                                                                     AlaPheLeuGlyLeuGlyValValAspAsnAsnGlyAsnGlyAlaArgValGlnArgVal
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Sequence 352, Michael D.

APPLICANT: Retter, Marc W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 21012.455C15

CURRENT APPLICATION NUMBER: US/09/850,716A

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 440

SOFTWARE: FastSEQ for Windows Version 3.0
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LENGTH: 900
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APPLICANT: Bangur, Chaiteanya S.
APPLICANT: Fanger, Garry R.
APPLICANT: Fanger, Garry R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Ranger, Nall
APPLICANT: RANGER S.
APPLICANT: RANGER S.
APPLICANT: RANGER S.
APPLICANT: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT APPLICATION NUMBER: US/09/735,705
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FASISEQ for Windows Version 3.0
ELENGTH: 900
US-09-684-215A-18 (1-128) x US-10-017-754-1862 (1-822)
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Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S
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                                                                                                                                US-9-99.77 /05-33

Sequence 353, Application US/0989778

Patent No. US2002014714341

SEDERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fanger, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Peckhan, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Nobert A.
APPLICANT: Henger, Nell
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND INSTANCE
TITLE OF INVENTION: COMPOSITIONS AND INSTANCE
TITLE OF INVENTION: COMPOSITIONS AND INSTANCE
CURRENT FILICATION NUMBER: 2001-06-28

NUMBER OF SEQ ID NOS: 467

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 953

LENGTH: 900
                                                                                                                                                                                                                                                                                                                                                                                                                     900
128
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                        ThrLeuAlaGluGlyProProAla 128
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                                                                                                                                                                                                                                                                                                                                                                                                                     1.09e-70
653.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-353
                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                   RESULT 14
US-09-897-778-353
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                              101
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81 AspGlyAlagroIleAsnSerAlaThrAlaMetAlaAspAlaLeuAsnGlyHisHisPro 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 GTCGGGAGCĞCTCCGGCGGCAAGTCTCGGCATCTCCACCGGCGACGTGATCACCGCGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICCGATAACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC
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128
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                                                                                                                                                          APPLICANT: Foy, Teresa M.
APPLICANT: Foy, Teresa M.
APPLICANT: Garet, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Malos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Fan. Liqui
APPLICANT: Fan. Liqui
APPLICANT: Fan. Liqui
APPLICANT: Fan. Liqui
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: ComPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: ComPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210120.455C18
CURRENT APPLICATION NUMBER: US.10.7117,982
CURRENT APPLICATION NUMBER: US.002-04-05
NUMBER OF SEQ ID NOS: 484
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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382 ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 ThrLeuAlaĞluGlyProProAla 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACATTGGCCGAGGGACCCCCGGCC 405
                                                                                                ; Sequence 353, Application US/10117982
; Publication No. US20030138438A1
; GENERAL INFORMATION:
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100.00%
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Job time : 189.154 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-117-982-353
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Best Local Similarity:
Query Match:
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LENGTH: 900
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Sequence 4, Applil Sequence 822, App Sequence 27, App Sequence 1862, Ap Sequence 1862, Ap Sequence 1862, Ap Sequence 1877, App Sequence 1877, App Sequence 1877, App Sequence 834, App Sequence 1861, Ap Sequence 1861, Ap Sequence 351, App Sequence 
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0 US-09-849-626-1879

4 US-10-017-754-1879

4 US-10-017-754-1879

105-09-754-1874

105-09-759-143-44

105-09-759-143-822

105-09-759-143-822

105-09-759-143-822

105-09-759-143-822

105-09-759-143-822

105-09-759-143-822

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105-09-895-814-834

105-09-895-814-835

105-09-895-778-8351
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121-478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FASTERD for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-922-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1879, Application US/09902941 Patent No. US20020172952A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang, Tongtong
Watanabe, Yoshihiro
Johnson, Jeffrey C.
Retter, Marc W.
Marnerakis, Margarita
Carter, Darrick
Fanger, Gary R.
Vedvick, Thomas S.
Bangur, Chaitanya S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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LENGTH: 186
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APPLICANT:
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APPLICANT:
                                                                                                                                                                                           Command line parameters:
-MODEL-frame+_p2n.model.-Pxlp
-MODEL-frame+_p2n.model.-Pxlp
-Word_Comp2_1/USPTO_spool_p/US09684215/runat_05092003_072203_619/app_query.fasta_1.853
-Q-/cgn2_1/USPTO_spool_p/US09684215/runat_05092003_072203_619/app_query.fasta_1.853
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-TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX.CA.00
-MAXLEN-200000000 -USR-R-SOF684215_GCGN_1 1_130_@trunat_05092003_072203_619
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-LONGLOG -DEV_TTMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT=0.5
-FGAPOP-6 -FGAPEXT=7 -YGAPOP-10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1879, Ap
                                                                                                                                                                                                        5, 2003, 08:54:40; Search time 43.5517 Seconds (without alignments) 1584.308 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1: /cgn2_6/ptodata/1/pubpna/US07_PUBCCMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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6/gn2_6/ptodata/1/pubpna/US08_PUBCCMB.seq:*
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7/cgn2_6/ptodata/1/pubpna/US10B_PUBCCMB.seq:*
7/cgn2_6/ptodata/1/pubpna/US60_PUBCCMB.seq:*
                                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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                                                                                                                                                                                                                                                                                                                               US-09-684-215A-17
148
1 TAASDNFQLSQGGGFAIPIGQAMAIAGQI 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1537136 segs, 1149988732 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Xgapop 10.0 , Xgapex.
Ygapop 10.0 , Ygapext: 0.
Fgapop 6.0 , Fgapext 7
'an 6.0 , Delext 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length: 0
length: 2000000000
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Score Match Length DB
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Database :

148

٠ 9 Result

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Total number Minimum DB Maximum DB

Searched:

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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Johnson, Jeffrey C.
                                                                                                                                                                                                                                                                                                                                         Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-09-757-417-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-757-417-46
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.:
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                                                                                                                                                                                                                                          22 ACGCCCCCCCCCCATACTTCCAGCTGTCCCAGGTGGCCAGGGATTCGCCATTCCGATC
                                                                                                                                                                                                                                                                                                                                                                               Sequence 1879, Application US/09849626

Fublication No. US20020197669A1

GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya
APPLICANT: Fanger, Gary
APPLICANT: Wang, Aijun
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Longer, Anne
APPLICANT: Clapper, Jonathan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C16
CURRENT APPLICATION NUMBER: US/09/849,626
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 1926
SSOT NO NO 1879
LENGTH: 186
LENGTH: 186
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                          Conservative:
Mismatches:
Indels:
                                                                                                                                                                                       US-09-684-215A-17 (1-30) x US-09-902-941-1879 (1-186)
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                                                                                                                                                                                                                                                                                       21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
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US-10-017-754-1879
Sequence 1879, Application US/10017754
Publication No. US20030054363A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Henderson, Robert A. APPLICANT: Wang, Tongtong APPLICANT: Watanabe, Yoshihiro
                                                                     1.01e-16
148.00
100.00%
100.00%
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148.00
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        ; ORGANISM: Homo sapiens
US-09-902-941-1879
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                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                            Alignment Scores:
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Sequence 46, Application US/09757417
Patent No. US20020082216A1
GENERAL INFORMATION:
APPLICANT: Fory Thereas M.
APPLICANT: Houghton, Raymond L.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY, DIAGNOSIS AND MONITORING OF BREAST CANCER FILE REFERENCE: 210121.479C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ThralaalaSeraspasnPheGlnLeuSerGlnGlyGlyGlyGlyPheAlaIleProIle
     APPLICANT: Margarita
APPLICANT: Margarita
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: Andria
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121 478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SEQ ID NO 1879
LENGTH: 186
LENGTH: 186
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Matches:
Conservative:
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 399
TYPE: DNA
Retter, Marc W.
Marnerakis, Margarita
Carter, Darrick
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148.00
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100.00%
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148.00
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Best Local Similarity:
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Best Local Similarity:
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COMPUTER READABLE FORM:
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22 ACGCCCCCCCCTCCCATTACTTCCAGCTCCCAGGGTGGGCAGGGATTCGCCATTCCGATC 81
                                                                                                                                                                                                           APPLICANT: Filigy, Steven P.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Mang, Aijun
APPLICANT: Money, Jeffrey C.
APPLICANT: Money, Jeffrey C.
APPLICANT: MONEY, R. Alec
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY,
TITLE OF INVENTION: DIAGNOSIS AND MONITORING OF BREAST CANCER
FILE REFERENCE: 210121.47963
CURRENT APPLICATION NUMBER: US/10/042,945
CURRENT FILING DATE: 2002-01-08
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FASLESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 355
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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Matches:
Conservative:
Mismatches:
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                                    21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
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Skelky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
                                                                                                                                                     Sequence 46, Application US/10042945; Publication No. US20030045468A1
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Vedvick, Thomas S.
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Publication No. US20030143243A1
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100.00%
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COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Query Match:
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                                                                                                                                   US-10-042-945-46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                   RESULT 5
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Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald C.
Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              447
30
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 652-4900
TELEPHONE: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-684-215A-17 (1-30) x US-10-084-843-4 (1-447)
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APPLICATION NUMBER: US/10/084,843
FILING DATE: 25-Feb-2002
CLASSIFICATION: <ur>
CLASSIFICATION DATA:

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                                                                                                                                                                    APPLICATION NUMBER: US/09/072,967
FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Campos-Neto, Antonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 4, Application US/10193002; Publication No. US20030135026A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 447 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
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100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-822
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US-09-780-669-822
                                                                             Alignment Scores:
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LENGIH: 675
LENGTH: 675
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APPLICANT:
APPLICANT:
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APPLICANT:
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PEPLICANT: Hepler, Milliam

AITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427023

CURRENT APPLICATION NUMBER: US/09/759,143

CURRENT FILING DATE: 2001-01-12
              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                            447
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NAME: WAIL, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.417C9
TELECOMUNICATION INFORMATION:
TELEFAX: (206) 682-4900
TELEFAX: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARCTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 10-Jul-2002
CLASSIFICATION: GURNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
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Patent No. US2002002248A1
GENERAL INFORMATION:
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
                             CURRENT APPLICATION DATA:
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Kalos, Michael D.
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Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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SOFTWARE: FastSEQ for
SEQ ID NO 822
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Best Local Similarity:
Query Match:
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1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hural, John
APPLICANT: Horal, John
APPLICANT: McNeill, Patricla D.
APPLICANT: Houghton, Raymonian
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERBENCE: 21012.427024
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
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                                         Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
                                                                                                                                   US-09-684-215A-17 (1-30) x US-09-759-143-822 (1-675)
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         Length:
Matches:
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Matches:
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Hepler, William
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Vedvick, Thomas S
Carter, Darrick
Li, Samuel
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US-09-780-669-822
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                                   Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                                                                                             Alignment Scores:
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APPLICANT:
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                                                                                                                                                                   APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210.12.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: PASTERO for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
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Matches:
Conservative:
Mismatches:
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                            Indels:
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Fublication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Alang, Yuqiu
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carigh.
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                          ; Sequence 822, Application US/09822827; Patent No. US20020081680A1; GENERAL INFORMATION:
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Skeiky, Yasir A.W.
Hepler, William T.
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                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-822
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Best Local Similarity:
Query Match:
                                                                                                           US-09-822-827-822
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                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                                                             RESULT 10
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CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT APPLICATION DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
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Mismatches:
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Matches:
; CURRENT APPLICATION NUMBER: US/09/895,793;
; CURRENT FILING DATE: 2001-06-29;
; NUMBER OF SEQ ID NOS: 982;
; SEQ ID NO 822;
; SEQ ID NO 822;
; LENGTH: 675;
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-822
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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5. US20020193296A1
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Hepler, William T.
Henderson, Robert A.
Hural, John
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Vedvick, Thomas S
Carter, Darrick
Li, Samuel X.
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Query Match:
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US-10-012-896-822
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US-09-287-849-27
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                                                                                          22 ACGCCCCCGTCCCGATAACTTCCCAGCTGTCCCAGGGTGGGCAGGGATTCGCCATTCCCGATC 81
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERBNCE: 210.11.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NGS: 1033-1000-1000
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                                           US-09-684-215A-17 (1-30) x US-09-895-814-822 (1-675)
                                                                                                                               21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
 Indels:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
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Houghton, Raymond L.
Vinals y de Bassols, Carlota
                                                                                                                                                                                                                      Sequence 822, Application US/10144678A Publication No. US20030157089A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
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Watanabe, Yoshihiro
                                                                                                                                                                                                                                                                                                                                                                        Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Skeiky, Yasir A. W.
Hepler, William T.
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US-10-144-678A-822
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Best Local Similarity:
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Sequence 27, Application US/09287849

Patent No. US20020009459A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Oblion, Davin C.

APPLICANT: Alderson, Wark

APPLICANT: Campos-Nego, Antonio

APPLICANT: Conixa Coffporation

TITLE OF INVENTION: Edsion Protiens of Mycobacterium tuberculosis Antigens

TITLE OF INVENTION: and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fanger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Weagher, Madeleine Joy
ATTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121, 427C27
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Indels:
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Matches:
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CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOCIWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 822
LENGTH: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
Sequence 822, Application US/10012896
Publication No. US2002018351A1
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Milcham, Johnifer L.
APPLICANT: Milcham, Johnifer L.
APPLICANT: Jiang, Yughu
APPLICANT: Allocker, Susan L.
APPLICANT: Railocker, Susan L.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Dontick
APPLICANT: Carter, Dontick
APPLICANT: Carter, Dontick
APPLICANT: Li, Samuel X.
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Houghton, Raymond L.
Vinals de (Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
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Best Local Similarity:
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NAME/KEY: CDS
LOCATION: (1)..(693)
COTHER INFORMATION: bi-fusion protein Ral2-DPPD (designated Mtb24),
OTHER INFORMATION: reading frame 1
NAME/KEY: CDS
LOCATION: (2)..(700)
COTHER INFORMATION: reading frame 2
NAME/KEY: CDS
LOCATION: (3)..(701)
COTHER INFORMATION: reading frame 3
UCCATION: (3)..(701)
COTHER INFORMATION: reading frame 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:bi-fusion OTHER INFORMATION: protein Ral2-DPPD (designated Mtb24), reading OTHER INFORMATION: frame 1
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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FILE REFERENCE: 014058-009020US
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR PELICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
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                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Job time : 44.8851 secs
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Best Local Similarity:
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SEQ ID NO 27
LENGTH: 702
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AX369169 Sequence
AR169152 Sequence
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AX267848
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AX365960
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AX267860
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-MODEL-frame+_p2n.model -DEV-x1p
-Q-/cgn2_1/USPPQ_spool_p/US09664215/runat_05092003_072202_559/app_guery.fasta_1.853
-Q-/cgn2_1/USPPQ_spool_p/US09664215/runat_05092003_072202_559/app_guery.fasta_1.853
-DB-Genembl - QFWT-fastap -SUFFIX=-10000000_-LOOPCL=0 -LOOPCL=0 -LOOPCXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UUSFPWT-pto -NORM=ext -HERPSIZE=500 -MINIEND -MAXEEN=200000000
-USFPWTS-DIGGOORY - NORM=ext -HERPSIZE=500 -MINIEND -MAXEEN=200000000
-USFPWTS-DIGGOORY - NORM=0-0 - WAIT - DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                        5, 2003, 07:52:39; Search time 535.655 Seconds (without alignments) 2291.192 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                          5777422
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                        nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                      1 TAASDNFQLSQGGQGFAIPIGQAMAIAGQI 30
                                                                                                                                                                                                                                                                                                                                                                                      2888711 seqs, 20454813386 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                   BLOSUM62
Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext 0
Fgapop 6.0 , Fgapext 7
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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ALIGNMENTS

RESULT 1

em\_ph:\* em\_pl:\* em\_ro:\* em\_sts:\*

em\_un:\*

em\_pat:\*

Sequence Sequence Sequence

Sequence Sequence Sequence

PAT 20-APR-2002

Houghton, R.,

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Unclassified:
1 (bases 1 to 447)
Reed, S.G., Skelky, Y.A.W. and Dillon, D.C.
Compositions and methods for the prevention and treatment of M. tuberculosis infection
Patent: US 6950456-A 4 26-FEB-2002;
Location/Qualifiers
                                                                                                                                                                                                                                    Unknown.
Unclassified.
Unclassified.
Unclassified.
Unclassified.
Unclassified.
Unclassified.
Unclassified.
Unclassified.
Unclassified.

Red S.G., Skelky, Y.A.W., Dillon, D.C., Campos-Neto, A., F. Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for diagnosis of tuberculosis Patent: US 6338852-A 4 15-JAN-2002;
Location/Qualifiers
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Matches:
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Sequence 4 from patent US 6338852.
AR182442
AR182442.1 GI:20225649
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             US-09-684-215A-17 (1-30) 🛪 AR169152 (1-447)
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AR182442
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1 (bases 1 to 447)
Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of
             PAT 16-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT 17-DEC-2001
                                                                                                                           1 Wang,T., Watanabe,Y., Henderson,R.A., Johnson,J.C., Retter,M.W., Marnerakis,M., Carter,D., Fanger,G.R., Vedvick,T.S., Bangur,C.S., Mcnabb,A., Fanger,N., Switzer,A., Mcneill,P.D. and Clapper,J.D. Compositions and methods for the therapy and diagnosis of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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             DNA
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           AX369169 186 bp DN
Sequence 1879 from Patent WO0204514.
AX369169
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Matches:
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Patent: US 6290969-A 4 18-SEP-2001;
Location/Qualifiers
1. 44.---"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
                                                                                                                                                                                                                                       1. 186.
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_tref="taxon:9606"
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Sequence 4 from patent US 6290969.
AR169152 47169152.1 GI:17906927
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Location/Qualifiers
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BD006325
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Reed, S.G., Skelky, Y.A. W., Dillon, D.C., Campos-Neto, A., Houghton, R., Vedvick, T.S., Twardzik, D.R., Lodes, M.J. and Hendrickson, R.C.
Compounds and methods for diagnosis of tuberculosis
Patent: US 6458366-A 4 01-OCT-2002;
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Compounds and methods for immunotherapy and diagnosis of tuberculosis
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CORIXA CORPORATION (US)
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Sequence 4 from patent US 6458366.
AR233097.1 GI:27275533
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Sequence 4 from Patent EP1203817.
AX429596 GI:21540845
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PAT 31-JAN-2002
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ANTONIO CAMPOS
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PC C12N15/31,C07K14/35,C07K16/12,C12Q1/68,C12N15/62,G01N33/53 CC Strandedness: Single;
CC Topology: Linear;
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Reed, S.G., Skelky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R. and Lodes, M.J.
Compounds and methods for diagnosis of Tuberculosis
Patent: JP 2001500383-A 4 16-JAN-2001;
CORIXA CORP
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PN JP 201500383-A/4
PD 16-1AN-2001
PF 07-0CT-1997 JP 1998518432
STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, PI
NETO,
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DEFINITION

RESULT 8 BD006445

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ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL

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OS Unidentified

OS Unidentified

PN JP 2001517069-A/4

PN JP 2001517069-A/4

PD 02-0CT-2001

PF 30-AGG-1996 US 08/523436,22-SEP-1995 US 08/533634 PR

22-MAR-1996 US 08/620814,05-JUN-1996 US 08/659683 PR

12-JUL-1996 US 08/620814,05-JUN-1996 US 08/659683 PR

12-JUL-1996 US 08/620814,05-JUN-1996 US 08/659683 PR

PI STEVEN G REED, YASIR A W SKEIKY, DAVIN C DILLON, ANTONIO CAMPOS PI RAYMOND HOUGHTON, THOMAS H VEDVICK, DANIEL R TWARDZIK PC CIZNI5-31,C07K14/35,A61K38/16,C12N15/62,G01N33/569,C1201/68, PC CIZNI5-31,C07K14/35,A61K38/16,C12N15/12,C12R1:19)

CC Strandedness: Single;
CC TOPOLOGY: Linear;
CC TOPOLOGY: Linear;
CC COMPOUNDS and methods for immunotherapy and diagnosis of CC COMPONDED.
BD069285 447 bp DNA linear PAT 27-AUG-2002 Compounds and methods for immunotherapy and diagnosis of
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(Dasses 1 to 447)

(Dasses 1 to 447)

Red 5.G., Skelky, Y.A.M., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.H. and Twardzik, D.R.
Compounds and methods for immunotherapy and diagnosis of Patent: JP 2001517069-A 4 02-0CT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C12N1/21//A61K39/04,(C12N1/21,C12R1:19)
Strandedness: Single;
Topology: Linear;
Compounds and methods for immunotherapy and diagnosis of tuberculosis
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1 (bases 1 to 675)
Mashiki,Z. and Harada,J.
                                                                 BD069285.1 GI:22614888
JP 2001517069-A/4.
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AR261272
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                                                                                                                                                                        Compounds and methods for immunotherapy and diagnosis of Tuberculosis.
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Reed, S.G., Skeiky, Y.A.W., Dillon, D.C., Neto, A.C., Houghton, R., Vedvick, T.S., Twardzik, D.R. and Lodges, M.J.

Compounds and methods for immunocherapy and diagnosis of Compounds and methods for immunocherapy and diagnosis of Compounds and methods for immunocherapy and diagnosis of Company A 13-FEB-2001;

Datent: JP 2001501832-A 4 13-FEB-2001;

OS Unidentified PN JP 2001501832-A/4

PD JP 2001501832-A/4

PP 70-00T-1997 JP 1998518456

PR 11-00T-1996 US 08/730510,13-MAR-1997 US 08/818112 PI STEVEN G REED, YASIR A W SKEIKX, DAVIN C DILLON, PI ANTONIO CAMPOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G01N33/50,G01N33/60,G01N33/569,C12N1/19,C12N1/20,C12N1/21, PC
              MICHAEL J LODES

MICHAEL J LODES

C C12N15/31,CO7K14/35,A61K39/04,A61K48/00,A61K49/00,C12N15/62,PC

C C12N15/31,CO7K14/35,A61K39/04,A61K48/00,A61K49/00,C12N15/62,PC

C C12N13/50,G01N33/50,G01N33/569,C12N1/19,C12N1/20,C12N1/21,PC

C C12N1/21,C12R1:19)

C C Strandedness: Single;
CC Topology: Linear;
Location/Qualifiers

FH Key

Location/Qualifiers

FT source

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BD006445.1 GI:18634816
JP 2001501832-A/4.
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BASE COUNT

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PAT 26-OCT-2001

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FEATURES

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Xu.J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Aslos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T. and Henderson,R.A.
                                                                                                                                                                                                Compositions and methods for the therapy and diagnosis of prostate
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 822)
Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,
Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.
Compositions and methods for the therapy and diagnosis of lung cancer
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Matches:
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Sequence 1862 from patent US 6509448.
AR277645 GI:29711294
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Location/Qualifiers
1. 822
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CORIXA CORPORATION (US)
Location/Qualifiers
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Matches:
Sequence 822 from Patent W00173032.
AX267848
AX267848.1 GI:16516494
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197 c 190 g 12
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Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
     Negative pressure control apparatus for engine mounted in vehicle Patent: US 6321716-A 822 27-NOV-2001; Location/Qualifiers 1. 675
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="genomic DNA"
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                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CORIXA CORPORATION (US)
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Delop 6.0 , Delext
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Perfect score:
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Maximum DB
                                                                                                                                                                                                                                                                                                                                   Sequence:
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Appl Appl Appl App App App App

Sequence 356,

Sequence Sequence Sequence

Sequence 3 Sequence 3 Sequence 3

Sequence Sequence Sequence Sequence

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APPLICANT: Campos. Neto, Antonio
APPLICANT: Campos. Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
CORRESPONDENCE: 153
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CAPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                              5: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                    Sequence 4, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 CCITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
US-08-818-112-4
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Sequence 1862, App. Sequence 353, App. Sequence 353, App. Sequence 351, App. Sequence 351, App. Sequence 348, App. Sequence 348, App. Sequence 348, App.

US-08-818-112-4 US-09-1111-4 US-09-056-556-4 US-09-736-457-1862 US-09-643-457-1862 US-09-663-4518-353 US-09-643-597-351 US-09-664-4218-351 US-09-664-4218-351 US-09-6520-4128-351 US-09-598-419-348

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148 148 148 148 148 148 148

945 1012 1012 1464

4, Appli

Sequence 4 Sequence 4 Sequence 4

Sequence 4, Appli

Description

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB

Length

Query Match

Score

Result g

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/cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
/cgn2\_6/ptodata/1/ina/PcTUS\_COMB.seq:\*

Issued\_Patents\_NA:\*

Database :

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Alignment Scores:
Pred. No.:
Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08018111
; Sequence 4, Application US/08018111
; Patent No. 6338652
; GENERAL INFORMATION:
   APPLICANT: Skeiky, Yasir A.W.
   APPLICANT: Skeiky, Yasir A.W.
   APPLICANT: Oampos-Neto, Raymond
   APPLICANT: Houghton, Raymond
   APPLICANT: Houghton, Raymond
   APPLICANT: Vedvick, Thomas S.
   APPLICANT: Twardzik, Daniel R.
   TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
   TITLE OF INVENTION: 148
   CORRESPONDENCE: 148
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: SEED and BERRY LLP
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: SEED and BERRY LLP
   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALABLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31,392
RELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPRATION POS SEO ID NO: 4:
SEQUENCE CHARRACTERISTICS:
TENTORMATION:
TELEPHONE: AA7 base pairs
                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
             TELEFAX: (200) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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148.00
100.00%
100.00%
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Washington
COUNTRY: USA
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Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: Reed, Steven G.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Steiky, Yasir A.W.

STREET: StoiColimbia Center, 701 Fifth Avennament A.W.

CITY: Seattle
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COMPUTER: IBM PC compatible
COMPUTER: System; PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/09/056,556
CLASSIFICATION: APPLICATION: APPLICATION:
                                                                        Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09056556
Patent No. 6350456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IELEFRA: (206) 622-490.
IELEFRA: (206) 682-6031
INFORMATION FOR SEQ ID NO SEQUENCE CHAPA
9.5e-16
148.00
100.008
100.008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
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STRANDEDNESS: single
                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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1 ThralaalaSerAspAsnPheGlnLeuSerGlnGlyGlnGlyPheAlaIleProIle 20
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                                                                         APPLICANT: ENGES, GATY
APPLICANT: Vedvick, Tom
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Marc
APPLICANT: Reteer, Marc
APPLICANT: Reteer, Marc
APPLICANT: Reteer, Marc
APPLICANT: Fan, Ligun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478015
CURRENT FILIAGO APPE: 200121.478015
CURRENT FILIAGO APPE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Railos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Menderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-215A-17 (1-30) x US-09-736-457-1862 (1-822)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
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                    Wang, Tongtong
Bangur, Chaitanya
Ločes, Michael A.
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100.00%
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Fan, Ligun
                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-736-457-1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-643-597-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-643-597-353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1862
LENGTH: 822
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LENGTH: 900
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APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardaik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF WINBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTINE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILLNG DATE: 05-MAY-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447
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6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-736-457-1862
; Sequence 1862, Application US/09736457
; Patent No. 6509448
                                                                                                US-09-072-596-4
; Sequence 4, Application US/09072596
; Patent No. 6458366
                                                                                                                                                                             APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900 (205) EBEFRAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                               GENERAL INFORMATION:
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Pred. No.:
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                                                                               RESULT 4
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TYPE: DNA
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Ligun
APPLICANT: Fan, Ligun
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Skalky, Yasir A.W.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
SURRENT FILLING DATE: 2000-06-28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 333
LENGT: AND THE OFFICE O
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                                                                                                                                                                           US-09-684-215A-17 (1-30) x US-09-643-597-353 (1-900)
                                                                                                                                                                                                                                                                                                                                                       21 GlyGlnAlaMetAlaIleAlaGlyGlnIle 30
   Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 353, Application US/09606421B; Patent No. 6531315; GENERAL INFORMATION:
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; Patent No. 6509448
; GENERAL INFORMATION:
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Yedvilck, Tom
APPLICANT: Catter, Darrick
APPLICANT: Retter, Marc
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; ORGANISM: Homo sapiens
US-09-606-421B-353
                        Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
Query Match:
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22 ACGCCCCGTCCCGATACTTCCAGCTGTCCCAGGGTGGGCAGGGATTCCCATTCCCATC 81
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              APPLICANT: Fan, Liqun
APPLICANT: Wang, Aljun
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478615
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
ED ID NO 1861
LENGTH: 945
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Tanger, Gary R.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Windy, All and APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Morell, Particla D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 21011.455011
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT APPLICATION NUMBER: 2000-08-21
NUMBER OF SEA
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Matches:
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Mannion, Jane
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; ORGANISM: Homo sapiens
US-09-736-457-1861
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US-09-643-597-351
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SEQ ID NO 351
LENGTH: 1012
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Pred. No.:
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SEQ ID NO 348
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                                                                                                                                                                                                                                                    APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: L1, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Mang, Aljun
APPLICANT: ARGIN AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210.11.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT APPLICATION NUMBER: US/09/606,421B
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NOS: 358
LENGTH: 1012
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US-09-620-412C-348
Sequence 348, Application US/09620412C
Patent No. 6446234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
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Matches:
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CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 348
LENGTH: 1464
                                                               127 GGGCAGGCGATGGCGATCGCGGGCCAGATC 156
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                                                                                                                                                                        ; Sequence 351, Application US/09606421B
; Patent No. 6531315
                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Wancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Chlamydia trachomatis
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148.00
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; ORGANISM: Homo sapiens
US-09-606-421B-351
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Best Local Similarity:
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US-09-606-421B-351
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Alignment Scores:

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                                                                                                                                                              1 ThrAlaAlaSerAspAsnPheGlnLeuSerGlnGlyGlyGlyGhealaIleProIle
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Batent No. 6448234

GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DAGOOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7

CURRENT APPLICATION NUMBER: US/09/620,412C

CURRENT FILIAG DATE: 2000-07-20

NUMBER OF SEC ID NOS: 363

SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
                                                                                                                                                                                                                                                                                                                                                              PETENT NO. 6565856
GENERAL INFORMATION:
APPLICANT: Sheiky, Yasir A.W.
APPLICANT: Scheiky, Yasir A.W.
APPLICANT: Scheiky, Yasir A.W.
APPLICANT: Scheiky, Yasir A.W.
APPLICANT: Scheiky, Ansir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REPERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Chlamydia trachomatis
US-09-598-419-348
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LENGTH: 1557
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1 ThralaalaaSerAspAsnPheGlnLeuSerGlnGlyGlyGlnGlyPheAlaIleProIle 20
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Patent No. 6432916
GENERAL INFORMATION:
APPLICANT: Probst, Peter
APPLICANT: Skeiky, Yasir
APPLICANT: Skeiky, Yasir
APPLICANT: Fling, Steve
APPLICANT: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGGOSTS OF CHLAWYDIAL INFECTION
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: 0S/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
                                                                                                                                                                                                                                                                                                                       Sequence 332, Application US/09598419
Fatent No. 6565856
GENERAL INFORMATION:
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121 469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SEQ ID NO 332
ENOTH: 1557
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Matches:
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Matches:
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US-09-598-419-332
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Length:
Matches:
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FastSEQ for Windows Version 3.0/4.0
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                                                                                                             148.00
100.008
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ne : 20.0345 secs
                                     TYPE: DNA
ORGANISM: Chlamydia
                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                             US-09-556-877-188
                         1578
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            SEQ ID NO 188
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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(without alignments) 1406.846 Million cell updates/sec September 5, 2003, 08:27:24; Search time 518.276 Seconds US-09-684-215A-17 Perfect score: Sequence: Run on:

148 1 TAASDNFQLSQGGGGFAIPIGQAMAIAGQI 30 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

22781392 seqs, 12152238056 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL-frame+-pan.model -DEV-xlp
-MODEL-frame+-pan.model -DEV-xlp
-Q-/cgn2\_1/USPTO\_spool\_p/US09684215/runat\_05092003\_072202\_572/app\_query.fasta\_1.853
-Q-/cgn2\_1/USPTO\_spool\_p/US09684215/runat\_05092003\_072202\_572/app\_query.fasta\_1.853
-Q-/cgn2\_1/USPTO\_spool\_p/US09684215/runat\_05090002\_0 -LOOPEXT=0
-UNITS-blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-UNITS-blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-UNITS-blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45
-UNITS-blts -START=1 -END=-1 -MATRIX=000 -MAIL-DAXIEN-200000000
-USER=US09684215\_CGGN\_1\_1\_4575\_Grunat\_05092003\_072202\_572 -NCPU=6 -ICPU=3
-NO\_MANAP -LARGRQUERY -NGE\_SCORRS=0 -WAIT -DSPEDCOK=100 -LONGLOG
-EGAPONT=120 -WARN\_THEOUT=30 -THRENS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

EST:\*

Database :

em\_gss\_phg:\* em\_gss\_vrl:\* gb\_gssl:\* gb\_est3:\*
gb\_est4:\*
gb\_est5:\*
em\_estfun:\* em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\* em\_gss\_fun:\* em\_gss\_mam:\* em\_gss\_mus:\* em\_gss\_rod: em\_estom:\* em\_esthum:\* em\_estin:\* em\_estpl:\* em\_estro:\* em\_htc:\* em\_estba:\* em\_estmu:\* em\_estov:\* gb\_est2:\* gb\_htc:\* gb\_est1:\*

## 29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

cription	- A	BB	М	MTU2TA.	C040P04U	CM3-GNO	MTU2TA.	MTU4TA.	MTU4TA.	MTU4TA.	MTU4TA.	MTU4TA.	MTU6TR.	MTU6TR.	MTU6TR.	MTU6TR.	MTU2TA.	MTU2TA.	MTU2TA.	MTU4TA.	MTU6TR.	MTU6TR.	MTU6TR.	MTU6TR.	MTUSTR.	MTU6TR.	MTUSTR.	MTUSTR.	MTUSTS.	VECUBER	MTCITAL	MTU2TA.	MTU2TA.	MTU2TA.	31603 MTU2TA.	27769 MTU6TR.	28453 MTU6TR.	29036 MTU6TR.	819016 UA38BPC	64854 A069p72u	928113 MTU6TR.	929039 MTU6TR.	931564 MTU2TA.	A931687 MTU4TA.	10
۵	CB597827	BB077789	CB184974	CA930964	BI070561	BI055877	CA931030	CA931960	CA931997	CA932035	CA932108	CA932138	CA927770	CA928449	CA928493	CA928769	CA931116	CA931394	CA931501	CA931767	CA927636	CA928025	CA929028	CA927727	CA928142	CA927617	CA927744	CA927930	CA933902	BU824U/5	CA934513	CA931302	CA931312	CA931446	CA931603	CA927769	CA928453	CA929036	BU819016	64854	92811	92903	93126	93168	ALIGNMENTS
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EST 03-APR-2003 Mus musculus (house mouse)
Mus musculus
Mus musculus
Musculus
Musculus
Mumalia: Metasoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mummalia: Butheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus AGENCOURT\_12972312 NIH\_MGC\_178 Mus musculus cDNA clone IMAGE:30297156 5', mRNA sequence. CB597827.1 GI:29515683 EST. RESULT 1 CB597827/c LOCUS SOURCE ORGANISM ACCESSION VERSION KEYWORDS

REFERENCE

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases I to 238)
Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kail, C., Kawai, J., Kill, N.,
Kilyosawa, H., Kolima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.
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BB077789 RIKEN full-length enriched, adult male diencephalon Mus musculus cDNA clone 9330145E04 3' similar to AF178432 Homo sapiens BB077789
BB077789
GI:8642849
                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
Tobna Library Preparation: Mc B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM57 row: j column: 13
High quality sequence stop: 475.
Location/Qualifiers
L. 747
//organism="Must musculus"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
Unpublished
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Email: genome-resegsc.riken.go.jp,
URL:http://genome-resegsc.riken.go.jp,
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URL:http://genome-resegsc.riken.go.jp,
URL:http://genome-resegsc.riken.go.jp,
URL:http://genome-resegsc.riken.go.jp,
N. okazaki,Y. Muramargu,M. and Hayashizaki,Y.
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                                                                                                                                                                  Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Email: genome-reségsc.riken.qo.1p.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host-"DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="male"
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57.00
75.00%
45.00%
38.51%
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VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL COMMENT REFERENCE AUTHORS

DEFINITION

CB184974 RESULT 3

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ACCESSION

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Eukarycta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.

I (bases 1 to 343)
Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and Tsai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIO70561 351 bp mRNA linear EST 19-JUN-2001 CO40P04U Populus strain T89 leaves Populus tremula x Populus tremuloides cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ophyta; Tracheophyta;
core eudicots; rosids
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1 (bases 1 to 351)
Jansson,S., Bhalerao,R., Erlandsson,R., Bjorkbacka,H., Karlsson,J., Sterky,F., Gustafsson,P. and Lundeberg,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tsai C-J
Plant Elotech Research Center
Michigan Technological University, School of Forest Resources
                                                                                                                                                                                                                                                                                                    Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
Location/Qualifiers
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59 c 101 g 66 t
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Teknikringen 30, Stockholm S-10044, Sweden
Tel: 46 8 790 8287
Fax: 46 8 245452
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Conservative:
Mismatches:
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Populus tremula x Populus tremuloides
                                                       Populus tremuloides (quaking aspen)
Populus tremuloides
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CA930964.1 GI:27419444
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Contact: Erlandsson R
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CB184974
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Lee, J. S., Lee, H. S., Noh, E. W. and Choi, Y. I. Gene Expression Profilling of the Poplar Suspension Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                         /tissue_type="Suspension cell"
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55 c 97 g 63 t
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Biotechnology Team
Korea Forest Research Institute
44-3 Omockhun-dong, Suwon, 441-350, Korea
Tel: 82 31 290 1162
Fax: 82 31 290 1020
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                 US-09-684-215A-17 (1-30) x BB077789 (1-238)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         jasolee@foa.go.kr
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Seg primer: T3
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CA931030
CA931030.1
GI:27419510
EST.
Populus tremuloides (quaking aspen)
Populus tremuloides
Bukaryota: Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids: eurosids IZ Malpighiales; Salicaceae; Populus.
I (bases 1 to 370)
Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and Tsal
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Aspen apex cDNA Library Populus tremuloides cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished Contact Tsad.C-J
Contact: Tsad.C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources 6
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
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tion/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIO55877 366 bp mRNA linear EST 15-JUN-2001
CM3-GN0330-120201-735-e08 GN0330 Homo sapiens cDNA, mRNA sequence
BIO55877
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0330-
120201-735=e08&t3=2001-02-12&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 366.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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1. 351
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/clone_lib="Populus strain
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    Email: rikerl@biochem.kth.se.
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Eukarycta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.
                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.

I (bases 1 to 370)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Michigan Technological University, School of Forest Resources & Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
                                                                                                                                                                                                   Unpublished Contact: Tsai C-J
Contact: Tsai C-J
Plant Jiotech Research Center
Michigan Technological University, School of Forest Resources 6
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
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Unpublished
Contact: Tsai C-J
Plant Biotech Research Center
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       Populus tremuloides
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I (bases 1 to 370)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and.Tsai
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Unpublished
Contact: Tsal C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2915
Fax: 906 487 2915
Email: chtsalemtu.edu.
Location/Qualifiers
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/clone_lib="Aspen apex
/note="Organ: apex"
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I (bases 1 to 370)

Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and Isai
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CA932108
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/db_xref="taxon:3693"
/clone_lib="Aspen apex CDNA Library"
/note="Organ: apex"
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Populus tremuloides (quaking aspen)
Populus tremuloides
Bukaryotta, Väidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryotta, Wäidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudlcotyledons; core eudlcots; rosids; eurosids I Malpighiales; Salicaceae; Populus.

1 (bases 1 to 370)
Ranjan,P., Ko,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai
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MTU4TA.P27.D05 Aspen apex CDNA Library Populus tremuloides CDNA,
MRNA sequence.
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Populus tremuloides
Eukaryota; Waridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids
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Location/Qualifiers
1. 370
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I (bases 1 to 374)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai
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; eurosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 374)
Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai
                                                                      Contact: Taai C-J
Contact: Taai C-J
Plant Blotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2915
Fax: 906 487 2915
Email: chtsai@mtu.edu.
Location/Qualifiers
1. 374
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1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
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Plant Biotech Research Center
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I (bases 1 to 374)
Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and Tsai
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                                                                                                                                                                                                                                                                                      Michigan Technological University, School of Forest Resources & Environmental Science
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
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/organism="Populus tremuloides"
/mol_Lype="mRNA"
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